

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2005, 19:27:11 ; Search time 27 Seconds
(without alignments)
1607.176 Million cell updates/sec

Title: US-10-614-954-6
Perfect score: 2334
Sequence: 1 MAFKIQDLTGLQPLGLLSIY.....EDMDRLKADKWKYQAVYG 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2314	99.1	451	2 T43733	trichothecene 3-O-
2	962.5	41.2	474	2 S50957	probable membrane
3	151.5	6.5	459	2 T45576	anthranilate N-hyd
4	150.5	6.4	430	2 T46216	hypothetical prote
5	149.5	6.4	450	2 T45573	anthranilate N-hyd
6	149	6.4	648	2 T45574	hypothetical prote
7	146	6.3	443	2 T45574	anthranilate N-hyd
8	143	6.1	475	2 T45961	anthranilate N-ben
9	141.5	6.1	436	2 D86378	protein F21J9.8 [i
10	132	5.7	439	2 T52321	taxadienol acetyl
11	131.5	5.6	433	2 H84826	hypothetical prote
12	130.5	5.6	451	2 T00527	hypothetical prote
13	126.5	5.4	435	2 E71418	hypothetical prote
14	124.5	5.3	450	2 T48479	hypothetical prote
15	124	5.3	445	2 T10717	anthranilate N-ben
16	121.5	5.2	482	2 G84823	probable anthocyan
17	118.5	5.1	480	2 H86411	protein F1K23.12 [
18	118	5.1	450	2 T02368	hypothetical N-ben
19	117	5.0	442	2 T10718	anthranilate N-ben
20	115.5	4.9	446	2 T10711	anthranilate N-ben
21	115	4.9	838	2 T13102	probable minor tai
22	113.5	4.9	3436	2 S55659	tegument protein 6
23	113	4.8	440	2 T52320	10-deacetyl baccati
24	111.5	4.8	575	2 D64998	hypothetical prote
25	109.5	4.7	451	2 T01140	hypothetical prote
26	109	4.7	445	2 T10719	anthranilate N-ben
27	105.5	4.5	446	2 D71418	hypothetical prote
28	105	4.5	1825	2 C88400	protein H19W22.1 [
29	105	4.5	1825	2 T32828	hypothetical prote

30	104.5	4.5	464	2 T45612	N-hydroxycinnamoyl
31	104.5	4.5	1337	1 I38670	protein-tyrosine-p
32	104	4.5	1896	2 T08851	Down syndrome cell
33	103.5	4.4	458	2 T06313	hypothetical prote
34	102.5	4.4	762	2 E98121	hypothetical prote
35	102.5	4.4	810	2 D95256	ATP-dependent Clp
36	102	4.4	753	2 A86756	prophage pi2 prote
37	101.5	4.3	465	2 D86166	protein F21B7.12 [
38	101.5	4.3	904	2 S51299	hypothetical prote
39	101.5	4.3	7576	2 T17428	FK506 polyketide s
40	101	4.3	363	2 T08542	mitogen-activated
41	101	4.3	363	2 T51735	mitogen-activated
42	101	4.3	761	2 A53414	A-kinase anchor pr
43	100.5	4.3	963	2 T09911	probable serine/th
44	100.5	4.3	1868	2 S48938	hypothetical prote
45	100	4.3	461	2 H84644	hypothetical prote

ALIGNMENTS

RESULT 1

T43733
trichothecene 3-O-acetyltransferase [imported] - Gibberella zeae (subsp. graminearum)
C;Species: Gibberella zeae
A;Variety: subsp. graminearum
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43733
R;Kimura, M.; Matsumoto, G.; Shingu, Y.; Yoneyama, K.; Yamaguchi, I.
PEBS Lett. 435, 163-168, 1998
A;Title: The mystery of the trichothecene 3-O-acetyltransferase gene. Analysis of the res
A;Reference number: Z22654; MUID:98433864; PMID:9762900
A;Accession: T43733
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-451 <KIM>
A;Cross-references: UNIPROT:O42692; EMBL:AB011417; NID:g3724288; PIDN:BA333768.1; PID:g3
A;Experimental source: strain F15
C;Genetics:
A;Gene: Tril101

Query Match 99.1%; Score 2314; DB 2; Length 451;
Best Local Similarity 99.1%; Pred. No. 6e-168;
Matches 447; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1	MAFKIQDLTGLQPLGLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV	60
DB	1	MAFKIQDLTGLQPLGLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV	60
QY	61	KAEGISSEGNLTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAFMFENIIAPRK	120
DB	61	KAEGISSEGNLTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAFMFENIIAPRK	120
QY	121	TLPIGSGTGPDDBPKPVILLQLNFIKGLILTVNGQHGAMVGDVAILLLSKACRNDPF	180
DB	121	TLPIGSGTGPDDBPKPVILLQLNFIKGLILTVNGQHGAMVGDVAILLLSKACRNDPF	180
QY	181	TEEMTAMNLDKRTIVPYLNTYTGPEVDHVIKADVAGDAVLTPVSASWAFETSPKA	240
DB	181	TEEMTAMNLDKRTIVPYLNTYTGPEVDHVIKADVAGDAVLTPVSASWAFETSPKA	240
QY	241	MSELKDAATKTLDASTPKFVSTDDALSAFIWKSASRVRLRIDGSAFTFCRAVDARPAWG	300
DB	241	MSELKDAATKTLDASTPKFVSTDDALSAFIWKSASRVRLRIDGSAFTFCRAVDARPAWG	300
QY	301	VSNVYPLLQNNMTYHNSTTGTEANESLGATASRLRSELDPSASNRQTRGLATYLLHNPKD	360
DB	301	VSNVYPLLQNNMTYHNSTTGTEANESLGATASRLRSELDPSASNRQTRGLATYLLHNPKD	360
QY	361	SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPEVTRRPIPEPVSLMYFMPPKPD	420
DB	361	SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPEVTRRPIPEPVSLMYFMPPKPD	420

QY 421 GFCAALSRLDEMDRLKADKWKTYAQYVG 451
Db 421 GFCAALSRLDEMDRLKADKWKTYAQYVG 451

RESULT 2
S00957
probable membrane protein YLL063c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein L0549
C:Species: Saccharomyces cerevisiae
C:Date: 10-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S00957; S64815
R:Wedler, H.; Wambutt, R.
submitted to the EMBL Data Library, January 1995
A:Description: Sequence of a 37 kb DNA fragment from chromosome XII of Saccharomyces cerevisiae
A:Reference number: S00950
A:Accession: S00957
A:Molecule type: DNA
A:Residues: 1-474 <WED>
A:Cross-references: UNIPROT:Q12226; EMBL:Z47973; NID:G642313; PID:G642321
R:Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64792
A:Accession: S64815
A:Molecule type: DNA
A:Residues: 1-474 <WED>
A:Cross-references: UNIPROT:Q12226; EMBL:Z47973; NID:G642313; PID:G642321
R:Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64792
A:Accession: S64815
A:Molecule type: DNA
A:Residues: 1-474 <WED>
A:Cross-references: EMBL:Z73168; NID:G1360275; PID:G1360276; MIPS:YLL063c
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGP:AYTL
A:Cross-references: SGD:S0003986
A:Map position: 12L
A:Keywords: transmembrane protein
F:153-169/Domain: transmembrane #status predicted <TM>

Query Match 41.2%; Score 962.5; DB 2; Length 474;
Best Local Similarity 44.4%; Pred. No. 3e-65;
Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;

QY 6 QLDLTGLPGLLSIYQISLLYPSVSSQYPTIVSFEQGLKRFSEAVPWAGQVKG 65
Db 22 QLDLTGLPGLLSIYQISLLYPSVSSQYPTIVSFEQGLKRFSEAVPWAGQVKG 81

QY 66 SEGNTGTSTFVPPEDVRVVKDLRDDPSAPTIETGMRKAGYPMAMPDENIAPRK 124
Db 82 DEGNTGTSTFVPPEDVRVVKDLRDDPSAPTIETGMRKAGYPMAMPDENIAPRK 140

QY 125 GPQTG-PDDPKPVILLQNFILKGLITVNGQHGAMDMVGDQAVIRLL 183
Db 141 GNTIGMAKSGPVFAVQANFISGLVLTIVGQHNIDITQESIIINLKNKCHQKPFSD 200

QY 184 EMTAMNDRKTIYVPLENTYIGPEVD--HQIVKA--DVAGGDVAVLPVS-ASWAFPTSP 238
Db 201 ELLIGNIDKSKSLPFDL--TWEDPTIVLHVIVTSNTSGEKEQSCSNSTWYVEFA 259

QY 239 KAMSELKDAATKTLDASTKFSVSTDDALSAPFKSASRVRLERIDGSAFECRAVDARPA 298
Db 260 ISLQNLRIILAMQCTSGTKFSVSTDDIVTAFIKWSVSKARLSRLKPKTKNGLGRVAVDRKR 319

QY 299 MGVSNNYPGLLQNMVTHNSTIGIANESLGATASRLSELDPDPA--SMRQRTGLATYLN 356
Db 320 LGLPETYPGLLVNMTNTGSLKSLDHSGLVLAQIRKLDPKVFLVANTCALATLSR 379

QY 357 NPKDSNVSLTADAPSTSVMLSSWAKVGLWDYDFGLGKPEVTRPIPEPVESLYMFP 416
Db 380 CPDKTKVSIPOPTIDTISGINVSSWAKVGLYVDVDFNLGLGKPSVRPRISLESILYFNP 439

QY 417 KKPDPGFCAALSRLDEMDRLKADKWKTYAQYVG 451
Db 440 RSSRGEMVVALCLRDQWECINADKWTNYATHIG 474

RESULT 3

T45576
anthranilate N-hydroxycinnamoyl/benzoyltransferase-like protein - Arabidopsis thaliana
N:Alternate names: protein Fl1C1.140
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45576
R:Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; Maye
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23007
A:Accession: T45576
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-459 <BAR>
A:Cross-references: UNIPROT:Q9SND7; EMBL:AL132976
A:Experimental source: cultivar Columbia; BAC clone Fl1C1
C:Genetics:
A:Map position: 3
A:Introns: 445/3
A:Note: Fl1C1.140

Query Match 6.5%; Score 151.5; DB 2; Length 459;
Best Local Similarity 22.5%; Pred. No. 0.0011;
Matches 95; Conservative 64; Mismatches 189; Indels 75; Gaps 17;

QY 4 KIQLDTGLPGLLSIYQISLLYPSVSSQYPTIVSFEQGLKRFSEAVPWAGQVKG 61
Db 24 KIHL-TPSDLSLLYLYNQPSLLFP---KPYETRFISRLKSSLSLTSLEIYFPLAGRLV 78

QY 62 AEGISEGNTGTSTFVPPEDVRV-VVKDLRDDPSAPTIETGMRKAGYPMAMPDENIAPRK 120
Db 79 KVNNEHNT-VSFYDCDDGCGVKFHAIESVSV-----SDILQPHG 120

QY 121 TLP-----IGPQTGPD-----PKPVILLQNFILKGLITVNGQHGAMDMVGDQAVIRLL 171
Db 121 SVPDFRLLFPFPMNGVRSIDGLSEPLALQVTEIKGIVISFGVNLVADGSSWNNFIHVM 180

QY 172 SKACRNDPTEEMTAM-----NLDKRTIYVPLENTYIGPEVDHQIVKADVAGDAVLT 225
Db 181 SKLCLNGWEIHQPLVLRGWFNDLDFPIHIP-----ASEIETEARNR 224

QY 226 PVSASWAFPTSPKAMSELKDAATKTLDASTKFSVSTDDALSAPFKSASRVRLERIDGSA 285
Db 225 EVSTKERVPHFTKEKLSLDKAKANDEIGSSDIKISLQAVLAHLWRSI--VRHSLNQEE 282

QY 286 PTEFCRAVDARPAWG--VSNNYPGLLQNMVTHNSTIGIANESLGATASRLSELDPASM 343
Db 283 ESRCGVAADFRQLNPPLDKCFGNVANGLTATVGDLLDRGLGWAALQINK-----TV 337

QY 344 RQRT-RGLATYLN--NPDKSNVSLTAD-ADPSTSVMLSSWAKVGLWDYDFGLGKPE 398
Db 338 RLHTNENFTFSSENVRNGKIPRIDVSRMGDGFVSNSPFQV-----YDNDFGLGKPM 393

QY 399 TVR 401
Db 394 AVR 396

RESULT 4
T46216
hypothetical protein T8P19.230 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46216
R:Choise, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sai
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23008
A:Accession: T46216
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-430 <CHO>
A:Cross-references: UNIPROT:Q9SMM7; EMBL:AL133315
A:Experimental source: cultivar Columbia; BAC clone T8P19
C:Genetics:

A:Map position: 3
A:Introns: 144/3
A:Note: T8P19.230
C:Superfamily: Arabidopsis CER2 protein

Query Match 6.4%; Score 150.5; DB 2; Length 430;
Best Local Similarity 20.3%; Pred. No. 0.0012; Indels 149; Gaps 19;
Matches 95; Conservative 61; Mismatches 163;

QY 25 LYPVSDSSQYPTIVTFEQL-----KRFSEAPW---V 56
DB LIPPVSETPNGHYLSNLDQNIALLVTKLYYKESRTQESNVVKKSLSEVLVHYYPV 75
QY 57 AGQ--VKAG--ISEGNTGTSFIVPFEDPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFDE 113
DB AGRLTISPGKIAVNCTGEGVVV-VEAEANCIGDITKEAISENRMETLEKLVY----- 127
QY 114 NIIAPRKTIPIGPGTDPDPKPVILLQLNFIKGLILTVNGQHGAMDMVGDQAVIRLLSK 173
DB DVGARNILEI-----PPVVQVTFKCGGVLGLGMSHMFQGV---AAAEFLNS 175
QY 174 ACRN-----DPFTEEMTAMNLDKTIIVPLENYTIGPEVDHQIVKADVAGGDAVLT 225
DB WCEMAGLPLSPVPPFLDRITLRSRNPKEFFPNEFDEI-----EDISDTGKIYD 225
QY 226 PVSASWAFPTFSKAMSELKDAATKTLDASTKFKVSTDDALSAPIWKSASRVRLERIDGSA 285
DB EEKLIYKSLFPEPEKLEKIMAE--ENNKNKVSFQALTGLWKR----- 271
QY 286 PTEFCBAVDAP-----AMGVSNYPGLLON-----MYHNTSTIGELANE 325
DB -----CEALRFKQDQVKLFAADGRSRFIRLPQGYCGNGIVLTGLVTSSELVGNPLSH 327
QY 326 SLG-----ATASRLSELDPASMRQRTGLATYLNHNPDKSNVSLTADADPSVML 377
DB SVGLVKRLVELVDGFWRAMD-----YFVNRTRPSVWAT-----LII 366
QY 378 SSWAKVGLWDYDPLGLGRPETVRRPIPE-----PVESLMYFMPKPKD 420
DB TSWSKLTLLKLDFGWG-----EPVSGVGLPGREVILFLPSGDD 406

RESULT 5
T45573
anthranilate N-hydroxycinnamoyl/benzoyltransferase-like protein - Arabidopsis thaliana
N:Alternate names: protein Fl1C1.110
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45573
R:Barques, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May
submitted to the Protein Sequence Database, December 1999
A:Reference number: 223007
A:Accession: T45573
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-450 <BAR>
A:Cross-references: UNIPROT:Q9SNE0; EMBL:AL132976
A:Experimental source: cultivar Columbia; BAC clone Fl1C1
C:Genetics:

Query Match 6.4%; Score 149.5; DB 2; Length 450;
Best Local Similarity 21.2%; Pred. No. 0.0016; Indels 83; Gaps 19;
Matches 97; Conservative 71; Mismatches 207;

QY 20 YTGISLVYPSVSSQYPTIVTFEQLGRFSEA-VPWVAGQVKAEGISE-----GN 69
DB YPQGLLFSPKD-SDFHLIISRLKSLSLALEIYFPFAGRLVKTENLEDTVSFFIDCG 99
QY 70 TGTSTFIVPDEPRVVVKD-LRDDPSAPTIEGMRKAGYPMAMFDENIIAPRKTLPIPGT 128
DB 100 SGARFL--HTEAKSVSVSILQPDGSPV---DPLKYFFP----- 133

QY 129 GPDDPK-----PVILLQNFIFKGLIILTVNGQHGAMDMVGDQAVIRLLSKACRN---- 177
DB -ADDFPKSCDGVSLPLLIQVTEMKDGVFISFCYNHNVADGVSMWSFFDTWSKICSTGSCF 192
QY 178 --DPFTEEBETAMNLDKTIIVPLENYTIGPEVDHQIVKADVAGGDAVLTVPVSASWAFPT 235
DB NYKPLVLKGFLEGGIDYPIHVPVSEABRPSPREPSV-----PITKEW-IFH 239
QY 236 FSPKAMSELKDAATKTLDASTKF-VSTDDALSAPIWKSASRVRLERIDGSAPTEFCRAVD 294
DB FTKNISDLKAKANSEIASSSDLEVSLSQAVSAHMRSI--IRHSGVSRQKTHCRLLVD 297
QY 295 ARPAMGVSNYP---GLLQNTWYTHNS---TIGELANESLGATASRLSELDPASMRQRT 348
DB LRQRV---NPLEKDCFCGNMYLSAITTVBELLDRLGIGEAALQIR-KLVSSQTNETCK 352
QY 349 GLATYLNHNPDKSNVSLTADADPSVMSLSSWAKVGLWDYDFGLGLGKPETVRRPIPEPV 408
DB SFAEDWVRNIRKLNLSGIGSKV--GNTIVIASFRFEVYNKDF--GMGKPIAIRAGPSNSI 408
QY 409 ESIMYFMPKPKPDGEFCAALSLRDEQMDRLKADKEWTKY 446
DB NGKLSVFGISGSDVQAILWGDVIVKLLADLEFLEH 446

RESULT 6
T45575
hypothetical protein Fl1C1.130 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45575
R:Barques, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May
submitted to the Protein Sequence Database, December 1999
A:Reference number: 223007
A:Accession: T45575
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-648 <BAR>
A:Cross-references: UNIPROT:Q9SND8; EMBL:AL132976
A:Experimental source: cultivar Columbia; BAC clone Fl1C1
C:Genetics:

Query Match 6.4%; Score 149; DB 2; Length 648;
Best Local Similarity 22.5%; Pred. No. 0.003; Indels 94; Gaps 19;
Matches 88; Conservative 63; Mismatches 146;

QY 112 DENIAPRKTLPIGP-----GTGPD-----DPK-----PVILLQNFIFKGLIL 150
DB DTFVVAESKLSVSDILOPHGSPVDFMSHFFSIDVKSIYGLSEPLALQVTELKDGVFI 145
QY 151 TVNGQHGAMDMVGDQAVI-----RLISKACRNPPFTEEMTAMNLD-RKTIIVPLENYTIG 205
DB SFGYNH---MVADGASINWFFNTWSKICSE-----YDQKNLKLPLVLRGWFL 190
QY 206 PEVDHQI-----VKADVAGGDAVLTVPVSASWAFPTSPKAMSELKDAATKTLDASTKPVST 261
DB DKIDYRIHIPASEADAPTSISQMPTSKERVFFHTKKNISLTKANGETSDDLIIS 250
QY 262 DDALSAPIWKSASRVRLERIDGSAPTEFCRAVDARPAAGVSNYP-----GLLQNTWYH 315
DB LQALSALHMRSI--IRHSGMKREETHCKVAVDLRQL-----NPFLLDKSCFGVNNILGVA 304
QY 316 NSTIGELANESLGATASRL---RSELDPASMRQRTGLATYLNHNPDKSNVSLTADADP 371
DB TVTVGELLDEHIGWAALQISKVRSQTD-----EYKTFEAENWVNVKISKTAGGP 356
QY 372 STSV-----MLSSWAKVG-----LW-----DYDFGLGLGKPETVRRPIPEP--VE 409
DB GNSISGKLVFOGIEBEGSIDVHATLWCDVVLKLLADVEFMENIKSEEDLLREQERKRRIE 416

QY 410 SLMYFMPKPKDGFCAALSLRDEMDRLKAD 440
Db 417 KLRKFW--RPRTSL--RSIVQREKDGKMSSE 444

RESULT 7
T45574
anthranilate N-hydroxycinnamoyl/benzoyltransferase-like protein - Arabidopsis thaliana
N:Alternate names: protein F11C1.120
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45574
R:Barques, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23007
A:Accession: T45574
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-443 <BAR>
A:Cross-references: UNIPROT:Q9SND9; EMBL:AL132976
A:Experimental source: cultivar Columbia; BAC clone F11C1
C:Genetics:
A:Map position: 3
A:Note: F11C1.120

Query Match 6.3%; Score 146; DB 2; Length 443;
Best Local Similarity 22.6%; Pred. No. 0.0028;
Matches 103; Conservative 62; Mismatches 204; Indels 86; Gaps 19;

QY 20 YTIQSLILPVSDSSQPTIVSTPEQGLKRFSEAVPWVAGQV--KAEG-----ISEGN 69
Db 39 YIQGLLFPKDPETH--FISRLTSLSSALDIYFPFAGRLNKVENHEDETVSFYINC DG 96
QY 70 TGTSTFTVPEDVRVVVKD--LRDDPSAPTIEGMRKAGYPMAMDENIIAPRTKLPIGPGT 128
Db 97 SGAKFTHAVSD--SVSVSDLLRDPGVP---DPFRIFYPM-----NGV 134
QY 129 GPDD--PKPVILLQLQFIKGLLTIVNGOHGAMDMVGQDAVI-----RLLSKARN----- 177
Db 135 KSIDGSEFLALQVTEMDRGVIFGYNH----WVADGASVWNFFRTWSKICSNQOREN 190
QY 178 -DPFTEEMTAMNLDRTKIIPVLENYTIIGPEVDHQIVKADVAGGDVAVLPVSVASWAFPT 236
Db 191 LQPLALKGLFVDMGDFPIHIPVSDTETSPSRE-----LSPTFKE-RVPHF 235
QY 237 SPKAMSELKDAATKTLDASTKFTVSTDDALSAPFWKSASRVRLERIDGSAFTFCRAVDAR 296
Db 236 TKRNIISDLKAKVNGEIGLRDHKVSLSQAVSAHMRISI--IRHSGLNQBEKTRCFVAVDLR 293
QY 297 PAMGVSNVYFGLLQNTYH-----NSTIGETANESIGATASRLRSELDPASMRQTRG 349
Db 294 QRUN-----PPLDKFCFHVYNSVVTIVGELHDLGWAFLQINMLRSLNEDYRIY 348
QY 350 LATYLHN-NPDKSNVSLTADADPSTVSMVSSWAKVGLWDYDFGLGKGPETVRRPIFEFV 408
Db 349 AENWVNMKIQKSLGSKMTRD---SVIVSSSPRFEVDNDF--GWGKPIAVRAGFSNII 403
QY 409 ESLMYFMPKPKDGFCAALSLRDEMDRLKADKEW 443
Db 404 SGKLVFRFGTIEGICIDVHAFLLPDLVLVGLADVEF 438

RESULT 8
T45961
anthranilate N-benzoyltransferase-like protein - Arabidopsis thaliana
N:Alternate names: protein F7J8.190
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45961
R:Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Lem
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23018

A:Accession: T45961
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-475 <BEV>
A:Cross-references: UNIPROT:Q9LFB5; EMBL:AL137189
A:Experimental source: cultivar Columbia; BAC clone F7J8
C:Genetics:
A:Map position: 5
A:Note: F7J8.190

Query Match 6.1%; Score 143; DB 2; Length 475;
Best Local Similarity 19.7%; Pred. No. 0.0053;
Matches 103; Conservative 71; Mismatches 190; Indels 158; Gaps 20;

QY 9 TLGQLPGLLSIVTQIS-LLYPVSDSSQPTIVSTPEQGLKRFSEAVPWVAGQVKAEB---- 63
Db 28 SVSDLPMLSCHVIQKVLLTSPPPSFDLVSLLRSLSSLTSLFPALAGRFSTTPAGH 87
QY 64 -GISEGNTGTSFI-----VPFEDVRVVVKDLRDDPSAPTIEGMRKAGYPM 109
Db 88 ISIVCNDAGVDVFAASAKHVKLSLDVLLPGEDVP-----L 121
QY 110 MFDENIIAPRTKLPIGPGTDPDPKPVILLQLNFQIKGLLTIVNGOHGAMDMVG-----QD 165
Db 122 LFRFFVFERLVSYNG-----HHKPLAAVQVTELDHGVFIGCTVNHSTVDGTSFWMHFFN 175
QY 166 AVIRLLSKARNDPFTEEMTAMNLDRTKIIPVLENYTIIGPEVDHQIVKADVAGGDVAVLT 225
Db 176 TPADTVSGACK-----IKHLPDFSRHTVDFSPVLPVPFGGPRVTFF 216
QY 226 PVSASW--AFFTFSPKAMSELKDA-----TKTLDA----- 254
Db 217 DADQPLREIRIFHFSREATKLTQRTNNRVNGIETAVNDGRKCNGBEINGKITTVLDSFLNN 276
QY 255 -----STKFVSTDDALSAPFWKSASRVRLERIDGSAFTFCRAVDAR-----PAM----- 299
Db 277 KXSVDRTAEISSQSLSAQLMRSVTRAR--NLDPSKTTTFRMAVNCRHRLERPMDDPYFG 334
QY 300 GVSNNVYFGLLQNTYHNTIGETANESIGATASRLRSEL---DPASMRQTRGLATYLHN 356
Db 335 NAIQSIPTL-----ASAGDLLSKDLSEAEQLHRNVVAHDDATVR---RGIAWESD 383
QY 357 -----NPDKSNVSLTADADPSTVSMVSSWAKVGLWDYDFGLGKGPETVRRPIFEFV 409
Db 384 PRLFFLGNPD-----GASITWGSSPRFMYDNDF--GWGKPLAVRSGGANKFD 429
QY 410 SLMYFMP-KKPDGEFCAALSLRDEMDRLKADKEWTKYAYV 450
Db 430 GKISAPFGREGNSVDLEVLAPETMTIGIENDAEFMQYVSEV 471

RESULT 9

D86378

protein F2109.8 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: D86378

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.P.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: D86378

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-436 <STO>

A:Cross-references: UNIPROT:Q9FYW1; GB:AE005172; NID:g9743331; PIDN:AAF97955.1; GSPDB:GN

C;Genetics:
A;Gene: F21J3.8
A;Map position: 1

Query Match 6.1%; Score 141.5; DB 2; Length 436;
Best Local Similarity 22.2%; Pred. No. 0.061;
Matches 74; Conservative 56; Mismatches 133; Indels 71; Gaps 14;

QY 135 PVLLQLNFK-GLILTVNGOHGMDVQDAVIRLLSKACRN-----DPFTE-----182
DB 135 PVLLIQANFPSCGLVITICVSHKTDATSLAMFIRGWAESSRGLGITLIPSTASEVFP 194
QY 183 ---EEMTAMNLDKRTIVPLENTYIGPEVDHQIKADVAGDAVLPVSNASWAFPTFSPK 239
DB 195 KPLDELPSKPMDRK-----EEVEE-----MSCVTKRFVFDAS 226

QY 240 AMSELKDAATKTLIDASTKFKVSTDDALSATFKWSASRVRLERIDGSAPTFCRAVDARPM 299
DB 227 KIKKRAKASRN---VKNPTRVEAVTALFWRCVTKV---SRLSLTP-----RTSVLIQILV 277

QY 300 GVSNNYPGLLQNNYHNTTIGEIANESLGATASRLSELDPASMRQRTGLATYLNHNP 359
DB 278 NLRGKVDLSLCEINTIGNMLSLMILKNEE--AAIERIQDVDEI---RRAKEIFSLNCKEMS 332

QY 360 KSNVSLTADADPSTV-----MLSSWAKVGLWDYDFGLGLCKPETYRRPIPEPVE 409
DB 333 KSSRFIFELLEETIGKYVYGRGNMDLWMSNCKGLGLYDADF--GWGKPVWVTGRTSHFK 390

QY 410 SLMYFMPKPDGEGFCAA--LSLRDEDMDRLKADKE 442
DB 391 NLMLLIDTK-DGEGIEAWITLLEQMSLFECDOE 423

RESULT 10
T52321
taxadienol acetyl transferase [imported] - Taxus cuspidata
C;Species: Taxus cuspidata
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52321
submitted to the EMBL Data Library, September 1999
A;Description: Molecular Cloning of a Taxa-4(20),11(12)-dien-5(alpha)-ol-O-Acetyl Transf
A;Reference number: Z26036
A;Accession: T52321
A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-439 <WAL>
A;Cross-references: UNIPROT:Q9M6F0; EMBL:AF190130; PIDN:AAF34254.1
C;Genetics:
A;Gene: TAT

Query Match 5.7%; Score 132; DB 2; Length 439;
Best Local Similarity 20.0%; Pred. No. 0.032;
Matches 90; Conservative 78; Mismatches 183; Indels 98; Gaps 21;

QY 5 IQDLTGLQPLGLSIVTQISLLYPVSDSSQYPIVST-----FEQGLKRFSEAVPWVAGQ 59
DB 27 LQLSSIDLNPVGRGSIFFNALLIYNASPS---PTMISADPAKPIREALAKILVYPPFAGR 83

QY 60 VK-----AEGISEGNTGTSIIVFPEDVPRVVVXDLRDDPSAPTEGMRKAGYPMAMF 111
DB 84 LRETENDGLEVECTGE---GAMFLEAMADNELSVLGDG---DDSNPSFQQL-----LF 130

QY 112 DENIAPRKTLPFGTGPDDPKPVLQLNFKLTKGGLITVNGOHGMDVQDAVIRLL 171
DB 131 -----SLPI--DTNFKDLILLVVQVTRFTFCGGFVGVCSFHGHVDCRGAAQFLKGL 179

QY 172 SKACRN-----DPFTEEMTAMNLDKRTIVPLENTYIGPEVDHQIKADVAGDAVLT 225
DB 180 AEMARGEVKLSLEPIWNRELKLD-DPKYLQPFHFEFLRAPSIVEKIQV-----227

QY 226 PVSASWAFPTFSPKAMSELKDAATKTLIDASTKFKVSTDDALSATFKWSASRVRLERIDGSA 285

DB 228 -----TYFIIDPETINYIKQS-----VMECKEFCSSFEVASANTW--IARTRAFQIPESE 276
QY 286 PTEFCRAVDARPMAGVSNYPGLLQNNYHNS--TIGEIANESLGATASRLRS-----ELD 339
DB 277 YVKILFGMDWR-----NSFNPLPSGYGNSIGTACAVDNVQDLSGLSLRAIMIIKKS 330

QY 340 PASMRQRTGLATYLNHNPDKSNVSLTADADPSTVMSLSSWAKVGLWDYDFGLGLKGPET 399
DB 331 KVSINDNFKSRVV---KPSELDNNHNE-----NVVAFADMSRLGDFEVDGFGWNAVSVS 383

QY 400 VRRPIPEPVESLM--YFM-----PKKPDG 421
DB 384 ---PVQQSALAMQNYFLFKPSKPKPDG 409

RESULT 11
H84826
hypothetical protein At2g40230 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84826
R;Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; 1998
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10611797
A;Accession: H84826
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-433 <STO>
A;Cross-references: UNIPROT:Q9XEF2; GB:AE002093; NID:g6598942; PIDN:AAF18737.1; GSPDB:GN
C;Genetics:
A;Gene: At2g40230
A;Map position: 2

Query Match 5.6%; Score 131.5; DB 2; Length 433;
Best Local Similarity 22.7%; Pred. No. 0.035;
Matches 67; Conservative 54; Mismatches 97; Indels 77; Gaps 17;

QY 135 PVLLQLNFK-GLILTVNGOHGMDVQDAVIRLLSKACRNDDPTEEMTAMNLD-DR 192
DB 137 PLVVQLTWIRDGGAALAVGVNHCVSDGIGSABFLTFELSK-DSLSQTELKRLHWD 195

QY 193 KTIQPY-LENTYIGPEVDHQIKADVAG-----GDVLTVPVSASWAFPTFSPKAMSELKD 246
DB 196 QLLMPSPIRDSLHPFNK---VPDLGCFVNRFAERLVPTSV-----VFERQKLNELKK 247

QY 247 AATKTLIDASTKFKVSTDDALSATFKWSASR-----VRL-----BRIDGSAPTEF- 289
DB 248 LASRLGEFNSKHTSP-EVLSAHVWRSWARSNLPSNQVLKLLFSVNRDRKPSLSPSGFY 306

QY 290 -----CRAVDARPMAGVSNYPGLLQNNYHNTTIGEIANESLGATASRLSELDPAS 342
DB 307 GNAFVVGCAQTIVKLTGKLSVATMLVQ-----AKERVG--DEYVRSVVEAS 354

QY 343 MRQRTGLATYLNHNPDKSNVSLTADADPSTVMSLSSWAKVGLWDYDFGLGLKGP 397
DB 355 -KERA-----SPDSVGV-----LILSQWSRLGLEKLDG--GLCKP 386

RESULT 12
T00527
hypothetical protein At2g19070 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T20K24.8
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00527; B84572
R;Roundley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, 1997
submitted to the EMBL Data Library, July 1997
A;Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.
A;Reference number: Z14167
A;Accession: T00527

A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-451 <R0>
A;Cross-references: UNIPROT:O64470; EMBL:AC002392; NID:g3176701; PID:g3176709
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84572
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-451 <STO>
A;Cross-references: GB:AE002093; NID:g3176709; PIDN:AAI2025.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g19070; T20K24.8
A;Map position: 2
A;Introns: 322/1

Query Match 5.6%; Score 130.5; DB 2; Length 451;
Best Local Similarity 21.1%; Pred. No. 0.044;
Matches 105; Conservative 64; Mismatches 195; Indels 119; Gaps 25;
QY 8 DTGQLPGLLSIYTOISLLYPVSDSQYPTIVSTPEQGLKRFSEAVPWVAGVYK-----61
Db 29 DQVGTTHIPTLY-----FYDKSESFQGNVVEILKTSLSRVLVHFPYMGRLRLWLPGR 83
QY 62 -----AEGI-----SEGNTGTFIVPPEDVPRVVVKDLRDPSPAPTIEGMRKAGYPMA 109
Db 84 FELNCNAEGVEFTEASEGK-----LSDFKDFSPTEFENL-----119
QY 110 MPDENIAPRKTLPIGGTGDDPKPVILLQLNFIK-GGLILTVNGHGMVQDADAVI 168
Db 120 MPQVYKNPIETIPL-----FLAQVTKFKCGGSLSVNVSHAIVD--GQSA-L 164
QY 169 RLLS-----KACRNDPFTTEEMTANLDRKTI---VPYLENTYIGPEVDHQ-----211
Db 165 HLISENGRLARGEPL-----TVFPLDKILWAGEP-LPPVSPPKFDKHEFDQPPFLIGE 219
QY 212 --IVKADVAGDVLTPVVSASWAFPTSPKAMELKDAA---TKTLASTKFTVSTDDALSA 267
Db 220 TDNVEERKKTIVVMLPLSTS-----OLOKRSKANGSKHSDPAKGF-TRYETVTG 269
QY 268 FINKSASRVLERIDGSAPEFCRAVDAPAM--GVSNNYPGLLQNMVYHNSHTIGIANE 325
Db 270 HVWRCAKARGH--SPQPTALGICIDTRSEMPPILPRGYFGNATLDVVAASTSGELISN 327
QY 326 SLGATASRLSELDPSMRQRTGLATYLHNPD-KSNVSLTA-----DADPSTSVN 376
Db 328 ELGFAASLSKAIKNVTNEYVMIGI-EYLKNQKDLKKFQDLHALGSTGPFYGNPNLGVV 386
QY 377 LSSWAKVGLWDYDFGLGKPEVTRRPIFEPVSLMYFMP-KKPDGEFCAALSIRDEMD 435
Db 387 --SWLTLPMTYGLDFGWG---KEFTGTGTHDFDGDLSILPDQNGDSVILATCLQVAHME 441
QY 436 RLK 438
Db 442 AFK 444

RESULT 13
E71418
hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)
A;Variety: Columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, R.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998

A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech,
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Falme, K.; Benes, V.; Rechman, S.; Ansc
C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thali
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: E71418
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-435 <BEV>
A;Cross-references: UNIPROT:O23393; GB:Z97338; NID:g2244870; PID:e336926; PID:g2244897
C;Genetics:
A;Map position: 4COP9-4G3845

Query Match 5.4%; Score 126.5; DB 2; Length 435;
Best Local Similarity 20.2%; Pred. No. 0.084;
Matches 99; Conservative 77; Mismatches 182; Indels 133; Gaps 26;
QY 4 KIOLDTIG-QLPGLLSIYTOISLLYP-VSDSQYPTIVSTPEQGLK-----RFGSEAVPWV 56
Db 23 RLQSLDLXCFG---IYVSTIFFYDLITSE-----VFSNKLKLSLSETLRFPY-L 72
QY 57 AGOVKAEGISEGNTGTSFIVPPEDVPRVVVKDLRDPSPAPTIEGMRKAGYPMAMPDENII 116
Db 73 AGRIEGLSISCNDEGAVTEARTD---LLLPDLRLNLTDSLSGF-----114
QY 117 APRKTLIP-IGPGTGDDPKPVILLQLNFI--KGLILTVNGHGMVQDADAVIRLLSK 173
Db 115 -----LPTLAAGESP-AAWPLLSVKVTFGSGGVAVSVSHKTCIDIASLVTFVK----164
QY 174 ACRNDPFTTEEMTANLDRKTIIVPLENTYIGPEVDHQIVKADVAGDVLTPVVSASWAF 233
Db 165 -----DWAT---TTAKGKSNSTI-EPAETIYPPSPHMYEQFPSTDSNIT---SKYVL 213
QY 234 --FTSPKAMSELK-DAATKTLDASTKFTVSTDDALSAFIWKA-----273
Db 214 KRFVPEPSKIAELKHAASESVVPVTRV---EATMSLIWRCARNSRSRNLIPQAVNM 269
QY 274 -----SHVRLERIDGSAPEFCRAVDAPAMGVSNNYPGLLQNMVYHNSHTIGETA 323
Db 270 QAMDILRLIPSPVAPKDVIGNIQSGFSLKXOABSEFEI-----PEIVATFRKNKERNEMI 325
QY 324 NESLGATASRLSELDPSMRQRTGLATYLHNPD-KSNVSLTA--ADPSTSV---MLSS 379
Db 326 KESLOG-----NTIGQSLLSLMAETVSESTIDRYMSS 359
QY 380 WAKVGLWDYDFGLGKPETV---RRPIFEPVSLMYFMPKPKPDGEFCAALSIRDEMDR 436
Db 360 WCKKPFYEYDF--GSGSPVWVGYSHTIYDNNMVGVLIDSKEGDG--VEAWISLPEEDMSV 416
QY 437 LKADKENTKYA 447
Db 417 FVDDQELLAYA 427

RESULT 14
T48479
hypothetical protein T28J14.20 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48479
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Len
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24493
A;Accession: T48479
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-450 <BEV>
A;Cross-references: UNIPROT:O9LYO7; EMBL:AL163652
A;Experimental source: cultivar Columbia; BAC clone T28J14
C;Genetics:
A;Map position: 5
A;Introns: 214/1
A;Note: T28J14.20

Query Match 5.3%; Score 124.5; DB 2; Length 450;
Best Local Similarity 19.0%; Pred. No. 0.13;
Matches 88; Conservative 71; Mismatches 190; Indels 113; Gaps 16;

QY 5 IOLDTIGQLPGLLSIYTOISLLYPVSDSQYPTIVSTPEQGLKRFSEAVPW--VAGQV- 60
DB 33 LSLSTLNDPYLELAKTIYVAPPSPNDVHDPASLFOQAL---SDALVYYYPPLAGKH 89
QY 61 -----KARGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYP 107
DB 90 RGSDDHRLRCSPEGV-----PFVRATADCTLSSNLKLD----- 126
QY 108 MAMFENIITAPKTLPIGPGTDPDPKPKVILLQNLFIKGLIITVNGHGAMDMVGQDAV 167
DB 127 ---MDTDLX---QLVPCDVAAPSGDYNPLALQITLPAACGLTATLASHSLCDGFGCASOF 180
QY 168 IRLSKACRNDPTEBEEMTAMNLDRTKIYVYLE---TKFVSTDDALSAPIWKSASRVRLERIDGSA 285
DB 181 FKTLE-----LAAGKTQPSIIPVMDRHLTSNNFSLNDQVBEQAPKLVDG 228
QY 221 DAVLTIVSASWAFFTSPKAMSEL---KDAATKTLDDASTKFVSTDDALSAPIWKSASRV 276
DB 229 EAC---SSATSPYTPSNDMVCEILNVTSEDITQLKEKVGAVVTTLEILAAHVWRAR--- 282
QY 277 RLERIDGSAFTFCRAVDARP-----AMGVSNYPGLLQNMVYHNSTI-----G 320
DB 283 -----CRALKLSPDQTSFLFGMAVGIRRIPEPPLPEGYGNAFVKANVAMKAG 329
QY 321 ETANESLGATASRLSELPASMRQTRGLATYLNHNPKSNVSLTADADPSTSVMLSSW 380
DB 330 ELSNPSLHVQLIKEAKKAA---QEKRYVLEQLRETEKTLKNNVACBEGGKAFMLLTDM 386
QY 381 AKVGLMD-YDFGLGLGKPKETVRRPIPEPVESLMYFMPKKPDG 421
DB 387 RQGLLDEIDFGVGSVNIIPLVPKYLP--DICIFLPRKQG 426

RESULT 15
anthranilate N-benzoyltransferase (EC 2.3.1.144) (clone pchbct1) - clove pink
N:Alternate names: anthranilate N-hydroxycinnamoyl/benzoyltransferase
C:Species: Dianthus caryophyllus (Clove pink)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10717
R:Yang, Q.; Reinhard, K.; Schiltz, E.; Matern, U.
Plant Mol. Biol. 35, 777-789, 1997
A:Title: Characterization and heterologous expression of hydroxycinnamoyl/ benzoyl-CoA:anthranilate N-benzoyltransferase
A:Reference number: Z17095; MUID:98088004; PMID:9426598
A:Accession: T10717
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-445 <YAN>
A:Cross-references: UNIPROT:O24645; EMBL:Z84383; NID:G2239082; PIDN:CAB06427.1; PID:G2239082
C:Function:
A:Description: catalyzes the synthesis of anthranilate
A:Pathway: phytoalexin biosynthesis
C:Keywords: acyltransferase; coenzyme A

Query Match 5.3%; Score 124; DB 2; Length 445;
Best Local Similarity 19.6%; Pred. No. 0.13;
Matches 93; Conservative 79; Mismatches 176; Indels 126; Gaps 23;

QY 20 YTOISLLYPVSDSQ---YPTIVSTPEQGLKRFSEAVPW--VAGQVKAEG---ISE 67
DB 37 HTGAVLIYKQPNNDNIHPSSSMYPDANILIALSKALVPPFPYPMAGRLKINGDRYEIDC 96
QY 68 GNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENIITAPKTLPIGPG 127
DB 97 NAEALFV---EAESHVLEDFCD--FRNDE-LHRVMVPTCDYSKGI----- 138
QY 128 TGPDDPKPVILLQL-NFIKGGIILTVNGHGAMDMVG-----QDAV 167

Search completed: January 23, 2005, 19:49:36
Job time : 31 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 23, 2005, 17:48:28 ; Search time 85 Seconds
(without alignments)
1903.375 Million cell updates/sec

Title: US-10-614-954-6
Perfect score: 2334
Sequence: 1 MAPKIQDITGLQPLLSIY.....EDMDRLKADKWTKYAQYVG 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2334	100.0	451	3	AAB03935 Trichothe
2	2334	100.0	451	8	Adn37286 Trichothe
3	2314	99.1	451	3	AAY51848 F. gramin
4	1860.5	79.7	459	3	AAB03934 Trichothe
5	962.5	41.2	474	3	AAB03936 Sequence
6	356.5	15.3	480	7	Adn81195 Orf11, SE
7	175	7.5	439	8	Ado70367 Barley ag
8	170.5	7.3	424	3	AGI18711 Arabidops
9	170.5	7.3	433	3	AGI18710 Arabidops
10	170.5	7.3	433	8	Ado70389 Unidentif
11	170.5	7.3	436	6	Abu58179 Wheat str
12	170.5	7.3	450	3	AGI18709 Arabidops
13	169.5	7.3	424	3	AGI48446 Arabidops
14	169.5	7.3	433	3	AGI48445 Arabidops
15	169.5	7.3	433	5	ABB93749 Arabidops
16	169.5	7.3	449	3	AGI48444 Arabidops
17	168.5	7.2	446	6	ABU58173 Arabidops
18	165.5	7.1	333	8	Ado70372 Barley ag
19	161	6.9	439	6	ABU58177 Soybean s
20	158.5	6.8	353	8	Ado70385 Barley ag
21	157.5	6.7	353	8	Ado70369 Wheat par
22	156.5	6.7	442	5	ABU93641 Arabidops
23	154.5	6.6	431	3	ABU36457 Arabidops
24	154	6.6	428	3	AGI484209 Arabidops
25	154	6.6	440	3	AGI484208 Arabidops

26	151.5	6.5	448	2	AAW04724 Aromatic
27	151.5	6.5	459	5	ABB92609 Herbicida
28	149.5	6.4	450	5	ABB92606 Herbicida
29	149	6.4	648	5	ABB92608 Herbicida
30	146	6.3	443	5	ABB92607 Herbicida
31	143	6.1	441	3	AAG46685 Arabidops
32	143	6.1	441	5	ABB93668 Arabidops
33	143	6.1	457	3	AAG46684 Arabidops
34	143	6.1	475	5	ABB93310 Herbicids
35	143	6.1	475	8	Adn72453 Thale cre
36	142.5	6.1	426	3	AGI37735 Arabidops
37	142.5	6.1	426	3	AGI37720 Arabidops
38	142.5	6.1	426	5	ABB93930 Herbicida
39	142.5	6.1	438	3	AGI37734 Arabidops
40	142.5	6.1	442	3	AGI37719 Arabidops
41	142	6.1	448	4	AAE00254 Taxus cus
42	142	6.1	448	7	ADB91967 Acyltrans
43	141.5	6.1	436	5	ABB91119 Herbicida
44	141.5	6.1	436	7	ADB91973 Acyltrans
45	138.5	5.9	327	3	AAG46686 Arabidops

ALIGNMENTS

RESULT 1
AAB03935
ID AAB03935 standard; protein; 451 AA.
XX
AC AAB03935;
XX
DT 12-SEP-2003 (revised)
DT 26-FEB-2001 (first entry)
XX
DE Trichothecene resistance polypeptide.
XX
KW Tricothecene resistance; resistant; crop protection; mycotoxin; fungus;
KW wheat; maize; barley; rice; heterologous gene; transformation; Fusarium.
XX
OS Gibberella zeae.
XX
PN WO2000060061-A2.
XX
PD 12-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-EP002769.
XX
PR 31-MAR-1999; 99US-00282995.
PR 11-FEB-2000; 2000US-00502852.
(NOVS) NOVARTIS AG.
(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PI Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;
XX
XX WPI; 2000-679374/66.
DR N-PSDB; AAA54209.

XX Plant cell for preventing mycotoxin contamination of wheat, maize, barley
or rice plant, comprises heterologous polynucleotide encoding gene
product expressed in cell, having tricothecene resistance activity.
PS Claim 15; Page 49-50; 62pp; English.

XX A heterologous gene encoding a gene product which confers tricothecene
resistance can be used to transform plant cells to make them resistant to
fungal infection. The transformation method is useful for preventing
mycotoxin contamination of a plant, particularly a crop plant such as
wheat, maize, barley or rice, and for reducing and/or preventing the
growth of a fungus of the genus Fusarium that produces a tricothecene,
preferably comprising a C-3 hydroxyl group, by growing transformed crop
plants in an area which is moderate to severe fungal infestation.
CC (Updated on 12-SEP-2003 to standardise OS field)

```

XX      SQ      Sequence 451 AA;
Query Match      100.0%; Score 2334; DB 3; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.1e-213;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MAFKIQDLTGLQGLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGOV 60
DB      1  MAFKIQDLTGLQGLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGOV 60

QY      61  KAEGISGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENIIAPRK 120
DB      61  KAEGISGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENIIAPRK 120

QY      121  TLPIGGTGPDPPKPVILLQNLFIKGLLITVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180
DB      121  TLPIGGTGPDPPKPVILLQNLFIKGLLITVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180

QY      181  TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGDAVLTPVSASMAFFTFSPKA 240
DB      181  TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGDAVLTPVSASMAFFTFSPKA 240

QY      241  MSELKDAATKTLDASTKFSVSTDDALSAFIWKSASRVRLERIDGSAFTFCRAVDARPAWG 300
DB      241  MSELKDAATKTLDASTKFSVSTDDALSAFIWKSASRVRLERIDGSAFTFCRAVDARPAWG 300

QY      301  VSNNYFGLLQNMTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLNHNPDK 360
DB      301  VSNNYFGLLQNMTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLNHNPDK 360

QY      361  SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRPIFEPVSLMYFMPKCPD 420
DB      361  SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRPIFEPVSLMYFMPKCPD 420

QY      421  GEFCALSLRDEDMRLKADKEWTKYAQYVG 451
DB      421  GEFCALSLRDEDMRLKADKEWTKYAQYVG 451

RESULT 2
ADN37286
ID      ADN37286 standard; protein; 451 AA.
XX      ID
XX      AC      ADN37286;
XX      DT      15-JUL-2004 (first entry)
XX      DE      Trichothecene 3-O-acetyltransferase protein SEQ ID NO:30.
XX      KW      maternal tissue; plant seed; plant;
XX      KW      bifunctional alpha-amylase subtilisin inhibitor gene promoter;
XX      KW      alpha-amylase inhibitor promoter; ASI promoter; plant protectant;
XX      KW      virucide; vaccine; resistance; infection; Fusarium graminearum;
XX      KW      trichothecene 3-O-acetyltransferase; enzyme.
XX      OS      Gibberella zeae.
XX      PN      WO2004035790-A1.
XX      PD      29-APR-2004.
XX      PF      17-OCT-2003; 2003WO-AU001381.
XX      PR      17-OCT-2002; 2002AU-00952143.
XX      PA      (MOLE-) MOLECULAR PLANT BREEDING NOMINEES LTD.
XX      PA      (GRAI-) GRAINS RES & DEV CORP.
XX      PI      Furtado A, Henry RJ;
XX      DR      WPI; 2004-348462/32.
XX      DR      N-ESDB; ADN37285.

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XX      PT      Expressing nucleic acid or protein in a plant seed, useful in enhancing
PT      resistance of a plant against Fusarium graminearum and barley stripe
PT      mosaic virus, comprises expressing a bifunctional alpha-amylase
PT      subtilisin inhibitor promoter.
XX      PS      Claim 20; SEQ ID NO 30; 169pp; English.

XX      CC      The present invention describes a method for expressing nucleic acid or
CC      protein in the maternal tissue of a plant seed. The method comprises
CC      expressing isolated nucleic acid operably under the control of a
CC      bifunctional alpha-amylase subtilisin inhibitor (ASI) gene promoter that
CC      is operable in the maternal tissue. Also described: (1) a method of
CC      enhancing or conferring resistance of a plant against: (a) Fusarium
CC      graminearum (head scab); and (b) barley stripe mosaic virus (BSMV); (2)
CC      an isolated transformed wheat and barley seed that expresses isolated
CC      nucleic acid encoding respectively a plant defence protein and a BSMV
CC      coat protein or an inhibitory RNA that prevents, inhibits or reduces
CC      expression of a BSMV movement protein placed operably under the control
CC      of the ASI gene promoter where the seed exhibits enhanced resistance
CC      against Fusarium graminearum (head scab) and BSMV by virtue of the
CC      presence of the nucleic acid compared to an otherwise isogenic line that
CC      does not express the nucleic acid placed operably under the control of
CC      the ASI gene promoter; (3) a method of producing an immunogenic
CC      composition; (4) an immunogenic composition comprising the maternal
CC      tissue of a plant seed produced by a process that comprises performing
CC      the method of (1); (5) a method of enhancing the nutritional quality of
CC      bran or animal fodder; and (6) an isolated bran or maternal tissue of a
CC      seed produced by a process that comprises performing the method of (5).
CC      The composition has plant protectant and virucide activities, and can be
CC      used in vaccines. The method is useful in expressing nucleic acid or
CC      protein in the maternal tissue of a plant seed. The method and ASI gene
CC      promoter are useful in enhancing or conferring resistance of a plant
CC      against Fusarium graminearum and BSMV and in enhancing the nutritional
CC      quality of bran or animal fodder. The seed or bran product and
CC      composition are useful as an oral vaccine against infection in the
CC      gastrointestinal, respiratory and urogenital tracts. The present sequence
CC      represents the Fusarium graminearum (Gibberella zeae) trichothecene 3-O-
CC      acetyltransferase, which is used in the exemplification of the present
XX      invention.
XX      SQ      Sequence 451 AA;

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Query Match      100.0%; Score 2334; DB 8; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.1e-213;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MAFKIQDLTGLQGLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGOV 60
DB      1  MAFKIQDLTGLQGLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGOV 60

QY      61  KAEGISGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENIIAPRK 120
DB      61  KAEGISGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENIIAPRK 120

QY      121  TLPIGGTGPDPPKPVILLQNLFIKGLLITVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180
DB      121  TLPIGGTGPDPPKPVILLQNLFIKGLLITVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180

QY      181  TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGDAVLTPVSASMAFFTFSPKA 240
DB      181  TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGDAVLTPVSASMAFFTFSPKA 240

QY      241  MSELKDAATKTLDASTKFSVSTDDALSAFIWKSASRVRLERIDGSAFTFCRAVDARPAWG 300
DB      241  MSELKDAATKTLDASTKFSVSTDDALSAFIWKSASRVRLERIDGSAFTFCRAVDARPAWG 300

QY      301  VSNNYFGLLQNMTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLNHNPDK 360
DB      301  VSNNYFGLLQNMTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLNHNPDK 360

QY      361  SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRPIFEPVSLMYFMPKCPD 420

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Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFBPVESLMTFMPKKPD 420
QY 421 GFCAALSLRDEDMRLKADKEWTKYAQYVG 451
Db 421 GFCAALSLRDEDMRLKADKEWTKYAQYVG 451
RESULT 3
AA51848
ID AAY51848 standard; protein; 451 AA.
XX AC AAY51848;
XX DT 12-SEP-2003 (revised)
XX DT 09-JUN-2000 (first entry)
XX DE F. graminearum trichothecene 3-O-acetyltransferase protein.
XX KW Trichothecene 3-O-acetyltransferase; selective marker.
XX OS Gibberella zeae.
XX PN JP2000032985-A.
XX PD 02-FEB-2000.
XX PF 15-JUL-1998; 98JP-00200280.
XX PR 15-JUL-1998; 98JP-00200280.
XX PA (RIKA ) RIKAGAKU KENKYUSHO.
XX PA (YAMA/) YAMAGUCHI I.
XX DR WPI; 2000-274037/24.
XX DR N-PSDB; AAY51848.
XX PT Trichothecin 3-O-acetyltransferase gene useful as a selective marker in
XX PT gene manipulations in eukaryotic host cells.
XX PS Claim 1a; Page 18-19; 25pp; Japanese.
XX CC This invention describes a novel protein with trichothecin 3-O-
XX CC acetyltransferase activity. The gene is used as a selective marker in a
XX CC gene manipulation using eukaryote as the host cell. This sequence
XX CC represents the trichothecin 3-O-acetyltransferase isolated from Fusarium
XX CC graminearum. (Updated on 12-SEP-2003 to standardise OS field)
XX SQ Sequence 451 AA;
Query Match 99.1%; Score 2314; DB 3; Length 451;
Best Local Similarity 99.1%; Pred. No. 9e-212;
Matches 447; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 MAFKIQDLTGQLPGLLSIYQISLVPVSDSQYPTIVSTFEOGLKRFSEAVPWAGQV 60
Db 1 MAFKIQDLTGQLPGLLSIYQISLVPVSDSQYPTIVSTFEOGLKRFSEAVPWAGQV 60
QY 61 KAEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTIEGMRKAGYPMAFMDENIIAPRK 120
Db 61 KAEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTIEGMRKAGYPMAFMDENIIAPRK 120
QY 121 TLPFGTGPDDPKPVILLQLNFIKGLILTVNGQHGAMDMVQDQAVIRLLSKACRNDPF 180
Db 121 TLPFGTGPDDPKPVILLQLNFIKGLILTVNGQHGAMDMVQDQAVIRLLSKACRNDPF 180
QY 181 TEEEMTAMNLDRTIIVPYLENYITIGPEVDHQIVKADVAGGDVILTPVSASWAFFTSPKA 240
Db 181 TEEEMTAMNLDRTIIVPYLENYITIGPEVDHQIVKADVAGGDVILTPVSASWAFFTSPKA 240
QY 241 MSELKDAATKLTLDASTKFTVSTDDALSFAFWKSASRVRLERIDGSAFTFCRAVDARPMG 300
Db 241 MSELKDAATKLTLDASTKFTVSTDDALSFAFWKSASRVRLERIDGSAFTFCRAVDARPMG 300

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QY 301 VSNYPGLLQNMTHYHNSTTIGSIANESIGATASRLSELDPASMRQRTGLATYLHNPKD 360
Db 301 VSNYPGLLQNMTHYHNSTTIGSIANESIGATASRLSELDPASMRQRTGLATYLHNPKD 360
QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFBPVESLMTFMPKKPD 420
Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFBPVESLMTFMPKKPD 420
QY 421 GFCAALSLRDEDMRLKADKEWTKYAQYVG 451
Db 421 GFCAALSLRDEDMRLKADKEWTKYAQYVG 451
RESULT 4
AAB03934
ID AAB03934 standard; protein; 459 AA.
XX AC AAB03934;
XX DT 26-FEB-2001 (first entry)
XX DE Trichothecene resistance polypeptide.
XX KW Trichothecene resistance; resistant; crop protection; mycotoxin; fungus;
XX KW wheat; maize; barley; rice; heterologous gene; transformation; Fusarium.
XX OS Fusarium sporotrichioides.
XX PN WO2000060061-A2.
XX PD 12-OCT-2000.
XX PF 29-MAR-2000; 2000WO-EP002769.
XX PR 31-MAR-1999; 99US-00282995.
XX PR 11-FEB-2000; 2000US-00502852.
XX PA (NOVS ) NOVARTIS AG.
XX PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX PI Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;
XX WPI; 2000-679374/66.
XX DR N-PSDB; AAA54206.
XX PT Plant cell for preventing mycotoxin contamination of wheat, maize, barley
XX PT or rice plant, comprises heterologous polynucleotide encoding gene
XX PT product expressed in cell, having trichothecene resistance activity.
XX PS Claim 15; Page 46-48; 62pp; English.
XX CC A heterologous gene encoding a gene product which confers trichothecene
XX CC resistance can be used to transform plant cells to make them resistant to
XX CC fungal infection. The transformation method is useful for preventing
XX CC mycotoxin contamination of a plant, particularly a crop plant such as
XX CC wheat, maize, barley or rice, and for reducing and/or preventing the
XX CC growth of a fungus of the genus Fusarium that produces a trichothecene,
XX CC preferably comprising a C-3 hydroxyl group, by growing transformed crop
XX CC plants in an area which is moderate to severe fungal infestation
XX SQ Sequence 459 AA;
Query Match 79.7%; Score 1860.5; DB 3; Length 459;
Best Local Similarity 77.6%; Pred. No. 2e-168;
Matches 349; Conservative 50; Mismatches 50; Indels 1; Gaps 1;
QY 2 AFKIQDLTGQLPGLLSIYQISLVPVSDSQYPTIVSTFEOGLKRFSEAVPWAGQV 61
Db 11 SFDIELDIIGQQPPLLSIYQISLVPVSDSQYPTIVSTFEOGLKRFSEAVPWAGQV 70
QY 62 AEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTIEGMRKAGYPMAFMDENIIAPRK 121
Db 71 TEGISEGNTGTSKILPYEETPRLVVKDLRDDPSAPTIEGMRKAGYPMAFMDENIIAPRK 130

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QY 122 LPTGCTGDDPKPVLLQLNFIKGLILTVNGHGAMDMVGODAVIRLLSKACRNDPFT 181
 DB 131 LAIGPENGNDPKPVLLQLNFIKGLILTVNGHGAMDMVGODAVIRLLSKACRNEST 190
 QY 182 EBEEMTAMNLDKRTIVPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSAWAFPTFSPKAM 241
 DB 191 EBEISAMNLDKRTIVPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSAWAFPTFSPKAL 249
 QY 242 SELKDAATKTLDASTKFVSTDDALSFAFIWKSASRVRLERIDGSAPTEFCRAVDARPMGV 301
 DB 250 SELKDAATKTLDASSRFVSTDDALSFAFIWQTSRVRRLARLDASTPTTEFCRAVDMRGPVG 309
 QY 302 SNYPGCLLQNTYHNTSTIGEIANESIGATASRLRSELDPASRQRTGRGLATYLNHNPKDS 361
 DB 310 SSTYPGCLLQNTYHNTSTIGEIANESIGATASRLRSELDPASRQRTGRGLATYLNHNPKDS 369
 QY 362 NVSLTADADPSTVMLSSWAKVGLWDYDFGLGKPEVTRRPIFEFVESLMYFMPKPKPDG 421
 DB 370 SVSLTADANPSSIMLSSWAKVGCWEYDFGFLGKPEVRRPRFEPFESLMYFMPKPKPDG 429
 QY 422 EFCALSLRDEMDRLKADKWTYKAYQYVG 451
 DB 430 EFTASISLRDEMDRLKADKWTYKAYIG 459

RESULT 5
 AAB03936
 ID AAB03936 standard; protein; 474 AA.

AC AAB03936;
 XX

DT 26-FEB-2001 (first entry)

DE Sequence encoding trichothecene resistance polypeptide.

XX Trichothecene resistance; resistant; crop protection; mycotoxin; fungus;
 KW wheat; maize; barley; rice; heterologous gene; transformation; Fusarium.

XX Saccharomyces cerevisiae.

XX WO2000060061-A2.

XX 12-OCT-2000.

XX 29-MAR-2000; 2000WO-EP002769.

XX 31-MAR-1999; 99US-00282995.

PR 11-FEB-2000; 2000US-00502852.

XX (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Hohn TM, Peters C, Salmerton JM, Reed JN, Dawson JL;

XX WPI; 2000-679374/66.

XX N-PSDB; AAA54210.

XX Plant cell for preventing mycotoxin contamination of wheat, maize, barley
 PT or rice plant, comprises heterologous polynucleotide encoding gene
 PT product expressed in cell, having trichothecene resistance activity.

XX Claim 15; Page 51-52; 62pp; English.

XX A heterologous gene encoding a gene product which confers trichothecene
 CC resistance can be used to transform plant cells to make them resistant to
 CC fungal infection. The transformation method is useful for preventing
 CC mycotoxin contamination of a plant, particularly a crop plant such as
 CC wheat, maize, barley or rice, and for reducing and/or preventing the
 CC growth of a fungus of the genus Fusarium that produces a trichothecene,
 CC preferably comprising a C-3 hydroxyl group, by growing transformed crop
 CC plants in an area which is moderate to severe fungal infestation

SQ Sequence 474 AA;

Query Match 41.2%; Score 962.5; DB 3; Length 474;
 Best Local Similarity 44.4%; Pred. No. 1.4e-82;
 Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;

QY 6 QLDTLGQLPGLISYITQISLLYPVSDSQYPTIVSTFQGLKRFSEAVPWVAGQVKAEGI 65

DB 22 QLDILGQOPSLYKLYQCSYIRVPDPSAHDHIVNTLTRLGLETAKNFQWLAGNVVNEGA 81

QY 66 SSGNTGTSTFIIPFEDVPRVVKDLDDPSAPTEIEGRKAGYPMANFENIAPRKL-PI 124

DB 82 DEGNTGTTRIIVPSDKIP-LIVQDLREDLSAPTMDSEKADPEIYMLDKTAPCMTINPP 140

QY 125 GPGTG-PDDPKFVILLQLNFIKGLILTVNGHGAMDMVGODAVIRLLSKACRNDPFTTE 183

DB 141 GNTIGMAAKSGPVFAVQANFISGGVLVIVGQHNIMDTGQESIINLNKSKHQKPFSD 200

QY 184 EMTAMNLDKRTIVPYLENYTIGPEVD--HQIVKA--DVAGGDAVLTPVS-ASWAFPTFSP 238

DB 201 ELLIGNIDKSKSIPLFDE-TWEPDITLVHEIVETSRNTSGEKEQSCSSNSTWAVVEFSA 259

QY 239 KAMSELKDAATKTLDASTKFVSTDDALSFAFIWKSASRVRLERIDGSAPTEFCRAVDARPA 298

DB 260 ISLQNLRIILAMQTCSTGTFVSTDDITVAFIWKSVSRARLSRLKPKETKSNLGRAVDVRKR 319

QY 299 MGVSNNYPGCLLQNTYHNTSTIGEIANESIGATASRLRSELDPA--SMRQRTGRGLATYLNH 356

DB 320 LGLPETYPGLLVNMTFTGSLKSLDKSLGLVLAQIRKLDPKVFDLAINTCALATLLSR 379

QY 357 NPKDSNVSLTADADPSTVMLSSWAKVGLWDYDFGLGKPEVTRRPIFEFVESLMYFMP 416

DB 380 CPDKTKVSIPOPIDTLTSGIMVSSWAKVSLYDVFNLGLGPKPKSVRRPRFISLESIIYFMP 439

QY 417 KKPDEGFCALSLRDEMDRLKADKWTYKAYQYVG 451

DB 440 RSRGGMVVALCLRDQWECNLNADKEWNTYATHIG 474

RESULT 6

ADE81195

ID ADE81195 standard; protein; 480 AA.

AC ADE81195;

DT 29-JAN-2004 (first entry)

XX Orf11, SEQ ID 23.

XX ML-236B; HMG-CoA reducing enzyme; Orf11.

XX Penicillium citrinum.

XX JP2003116567-A.

XX 22-APR-2003.

XX 15-OCT-2001; 2001JP-00316578.

XX 15-OCT-2001; 2001JP-00316578.

XX (SANY) SANKYO CO LTD.

XX WPI; 2003-817677/77.

XX N-PSDB; ADE81194.

XX Novel DNA associated with synthesis of ML-236B, useful for improving ML-
 PT 236B production in ML-236B producing microbe.

XX Example 8; SEQ ID NO 23; 142pp; Japanese.

XX The present invention relates to a DNA sequence (I, ADE81173), which is
 CC associated with ML-236B synthesis. (I) is useful for improving ML-236B

CC production in a HMG-CoA reducing-enzyme-inhibitor ML-236B producing
 XX microbe. The present sequence was used to illustrate the invention.
 SQ Sequence 480 AA;

Query Match 15.3%; Score 356.5; DB 7; Length 480;
 Best Local Similarity 26.5%; Pred. No. 1.2e-24;
 Matches 129; Conservative 87; Mismatches 183; Indels 87; Gaps 20;

QY 25 LLYPVSDSSQYPTVTFEQLKRFSEAVPWAG---QVKAEGISEGNTGTSTFV---PP 78
 DB 20 LCPHSDAS-IPQTVSVLRGLSKVAKLLFLGNLQOVENAGLRFG---SPAVESNFS 74
 QY 79 EDVPRVVVKDLRDDPSAP---TIEGRKAGYPMWPMFDENIAPRKLPIGPGTGDPPKP 135
 DB 75 EP-PTLSVRDMTSGSDTWSWTYHDLRERGFPMSSLNRLDVLAP-----TDPGSGRT 124
 QY 136 VIL-LQNLFTKGLLITVNGQHGAMDMVGDAVIRLLSKACRNDPTEDEM----- 185
 DB 125 RLAAQANFIPGCLLYVSTSHAFADAGLSTLLCEWSQCRDALGTSDEIPNVSRQKEI 184
 QY 186 -TAMNLD---RTIV-PYLENYTIGPEVDHQIVKADVAGD-----AVLTPVS 228
 DB 185 STALDQDSPCRSLVQPYSPTSVAYERLKSXPILWHVLGDLWRPKERSRILMSQIPSP 244
 QY 229 ASWAFTTFPKAMSELKDA---TKTLDASTKPVSTDDALSAPFKWSASRVRL-ERIDGS 284
 DB 245 VRSCIFSIANSVEKLQVALGSSGVPKSSQSISTDALGALLSCLMRARLTERESFE 304
 QY 285 APTF--FCRAVDARPAMGVSNNYPG-----LLQNTYHNTSTIGEIANESLG 328
 DB 305 NPKAETMARVAVNRKLLSVPEHLGNTILYAVTKLSIDLATRGTOHLNVVAQSLRESL- 363
 QY 329 ATASRLRSELDPASMRQRTGLATYLHNNPKSNVSLTADADPSTSVMLSSWAKVGLWDY 388
 DB 364 -----DELRSMMQEAVELA---NNIPDVRCMGLSPFTWVAENNVFSSLSRLPLLDW 413
 QY 389 DFGL-----GLGKETVRRPIFEVSLMYPMPKPGDFCAALSDEDMDLKADKEWT 444
 DB 414 DFGSIGHGLGKPDNRFP-DKCFEGITFTMPQPDGSLIMITKAVDMWELMTDQTF 472
 QY 445 KYAQYV 450
 DB 473 EPPSFV 478

RESULT 7
 ADO70367
 AC ADO70367 standard; protein; 439 AA.
 XX
 AC ADO70367;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Barley agmatine coumaroyltransferase.
 XX
 KW barley; agmatine coumaroyltransferase; ACT; antimicrobial;
 KW pathogen resistance; enzyme.
 XX
 OS Hordeum vulgare.
 XX
 PN WO2004044195-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 11-NOV-2003; 2003WO-EP012601.
 XX
 PR 12-NOV-2002; 2002EP-00025076.
 XX
 PA (RISO-) RISO NAT LAB.
 XX
 PI Rasmussem S, Burhenne K, Kristensen B;
 XX

DR WPI; 2004-431667/40.
 XX N-PSDB; ADO70366.
 PT New polynucleotide encoding a polypeptide having agmatine
 PT coumaroyltransferase (ACT) activity, useful for establishing or enhancing
 PT a pathogen resistance in a plant, and for producing a biopolymer.
 XX Claim 1; Fig 1; 11pp; English.
 XX The present invention provides the protein and coding sequences of the
 CC barley agmatine coumaroyltransferase (ACT) enzyme. The sequences are
 CC useful for the preparation of an antimicrobial compound, its precursor or
 CC a plant protection composition, for establishing or enhancing a pathogen
 CC resistance in a plant, and for producing a biopolymer. The present
 CC sequence is the protein of the invention.
 XX Sequence 439 AA;

Query Match 7.5%; Score 175; DB 8; Length 439;
 Best Local Similarity 23.8%; Pred. No. 2.3e-07;
 Matches 118; Conservative 62; Mismatches 185; Indels 130; Gaps 26;

QY 2 AFKIQDLTLGQLPGLLSIVTOISLLYPVSDSSQYPTIVS-----TFEQGLKR 48
 DB 10 AVKPEVGACGLAPGCTADVPLITVL-----DKANFTYISVIYAFHAPAPNAVLEAGLR 65
 QY 49 -FSEAVPWVAGQ--VKAEG---ISEGNTGTSTFIVPEFDPVPRVVVKDLRDDPSAPTEGMR 102
 DB 66 ALVDYREM-AGRLGVDDASGGRAILLNDAGARFVEATADVALDSVMPLK-----PTSE--- 116
 QY 103 KAGYPMWPMFDENIAPRKLPIGPGTGDPPDPKPVILLQL-NFKKGLLITVNGQHGAMDM 161
 DB 117 -----VLSLHP-SGDDGPEELMLIQVTRFACGSLVGVFTTQHIVSDG 157
 QY 162 VGODAVIRLLSKACRN---DP-----FTEEMTAMNLDKRTI--VPYLENYTIGPE 207
 DB 158 RTGNPFFVAMSQATRGAAIDPVVHDRASFFHPREPLHVEYHRGVFEPY-----E 209
 QY 208 VDHQIV-KADVAGGDAVLTPVSASWAFTFSPKAMSELKDAATKTLDASTKPVSTDDALS 266
 DB 210 KAHDVVGAGDGEDEVVNVKH-----FSREFISKLAQASA---GAPRPCSTLQCVV 259
 QY 267 AFIWKSASRVRLERIDGSAPTEFCRAVDARPAMG--VSNNYPGLLQNTYHNTSTIGE-- 322
 DB 260 AHLWRSMTWAR--GLDGGETTSAIADVGRARMSQVDPDGTGNVILMARPTTAGELVT 317
 QY 323 -----ANESIGATASRL-----RSELDPASMRQRTGLATYLHNNPKSNVSLTADADP- 371
 DB 318 RPVKHAVELISREVARINDGYFKSFIDFAN-----SGAVEKERLVATADADM 365
 QY 372 --STSVMLSSWAKVGLWDYDFGLGLGKPKETVRRPIF-----EPVESLMYFMPK-KPDGEF 423
 DB 366 VLSPNIEVDSWLLIPFYDMDFGG-----RPFEPFMSYLPVEGLILLPSFLGDSV 417
 QY 424 CAALSRLDEDMRLK 438
 DB 418 DAYVPLFSRDMNTFK 432

RESULT 8
 AAG18711
 ID AAG18711 standard; protein; 424 AA.
 XX
 AC AAG18711;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 20229.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX

PR	15-SEP-1999;	99US-0154018P.	
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PR	20-SEP-1999;	99US-0154779P.	
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PR	23-SEP-1999;	99US-0155486P.	
PR	24-SEP-1999;	99US-0155659P.	
PR	28-SEP-1999;	99US-0156458P.	
PR	29-SEP-1999;	99US-0156596P.	
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PR	12-OCT-1999;	99US-0158369P.	
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PR	28-OCT-1999;	99US-0161920P.	
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PR	29-OCT-1999;	99US-0162142P.	
Query Match			7.3%; Score 170.5; DB 3; Length 424;
Best Local Similarity			23.4%; Pred. No. 5.8e-07;
Matches			107; Conservative 61; Mismatches 153; Indels 137; Gaps 25;
QY	36	PTIVSTF--EQGLKR-FSEA-VPW--VAGQVKAEG-----ISEGNTGTSFIYPPFEDVPRV	84
DB	35	PTGASNFFDPQVNMKEALSALVPFPYPMAGRLKRDDGRIEIDCNGAGVLFVW--ADTPSV	92
QY	85	VVKDLRDD--PSAPTEGMRKAGYPWMPDENIIAPRKLTP-IGPGTGDDPKPVLLOL	141
DB	93	I-----DDFGDFAPTL-----NL---RQLPEVDHSTGIHS-FPLVLQV	128
QY	142	NFIK--GGLILTNGQHGAMVQGDVIRLLSKACRNDPTEEMTAMNLDKRTIYPLYE	200
DB	129	TFPKCGASLGVGMHQAADGFSGLHFIWSDMAR-----GLD-----	167
QY	201	NTTIGEVNHOIVKA-----DVAGGDAVLTPVSASWAPFTFSPKAM	241
DB	168	-LTIPFIDRTLRLARDPPQAPHHVEYQAPSMKIPLDPSKSGPENTTVSIFKLTRDQL	226
QY	242	SELKDAATKTLDASTKFVSTDDALSAPFVKSASRVRLERIDGSAPEFCRAVDA----	297
DB	227	VALK--AKSKEDGNTVSYSYEMLAGHVRSVCKAR--GLPNDQETKLIATDGRSLRP	282
QY	298	AMGVSNYFCLLQNNYTHNSTI-----GEIANESLGATASRLRSELDPAS	342
DB	283	QLP-----FGYFGNVIFTATPLAVAGDLLSKPTWYAAGQIHDFLVRMDDNYLSALD---	334
QY	343	MRQRTGLATYLLHNPDKNVSLTADPSTSVMLSSWAKVGLWYDFGLGKPKETVR	402

Db	335	-----YLEMQPDLALVGAHTYKCPNLGITSWRLPIYDADFGWG-----R	376
QY	403	PIPE-----PVSRLMYFMPKCP-DGEFCAALSRLRDEDM	434
DB	377	PIFMGPGGIPYGLSVLPSPNTDGLSVAILQSEHM	414
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ID	AAG18710 standard; protein; 433 AA.		
XX	AAG18710;		
XX	17-OCT-2000 (first entry)		
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 20228.		
XX	Protein identification; signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		
KW	termination sequence.		
XX	Arabidopsis thaliana.		
OS	EP1033405-A2.		
PN	06-SEP-2000.		
PD	25-FEB-2000; 2000EP-00301439.		
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PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 7.3%; Score 170.5; DB 3; Length 433;

Best Local Similarity 23.4%; Pred. No. 6e-07; Indels 137; Gaps 25;

Matches 107; Conservative 61; Mismatches 153; Indels 137; Gaps 25;

QY 36 PTIVSTF--EQLKR-FSEA-VPW--VAGQVKAEG-----ISEGNTGTSTFIVPFEDVPRV 84

Db 44 PTGASNFFDPQWKEALSKALVPFPYPMAGRLKRDGRIEIDCNGAGLVFVV--ADTPSV 101

QY 85 VVKLRDD--PSAPTIEGMRKAGYPMAMFDENIIAPRKTLP-IGPGTGPDDEPKPVILLQL 141

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Db 102 i-----DDGDFAPTL-----NL-----QLIPEVDHSTGIHS-FPLLVLQV 137
QY 142 NFIK-GGLILTVNGQHGAMVQGDVIRLLSKACRNDPTEBEMTAMNLDKRTIIVPYLE 200
Db 138 TPFKCGASLGVGMQHAADGFGSLHFINTWSDMAR-----GLD----- 176
QY 201 NYTIGEVHDIQVKA-----DVAGDAVLTPVSASWAFTEFSPKAM 241
Db 177 -LTIPFIDRTLRLARDPPQAFHVEYQAPSMKIPLDPSKSGPENTTVSIFKLTRDQL 235
QY 242 SELKDAATKTLDASTKFSVSTDDALSAFIWKASRVLELIDGSAPEFCRAVDA-----RP 297
Db 236 VALK--AKSKEDGNTVSYSSYEMLAGHVRSVGKAR--GLPNDQETKLYIATDGRSLRP 291
QY 298 AMGVSNNYPGLLQNTYHNSTI-----GEIANESLGATASRLRSELDPAS 342
Db 292 QLP-----PGYFGNVIFTATPLAVAGDLLSKPTWYAAGQIHDFLVRMDNLYLSALD--- 343
QY 343 MRQRTGLATYLNHNPDKNSVLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRR 402
Db 344 -----YLEMQPDLGALVRGAHTYKCPNLGITSWVRLPIYDADFQWG-----R 385
QY 403 PIPE-----PVESLMYFMPKPK-DGEFCAALSRLRDEDM 434
Db 386 PIFMGPGGIPYEGLSFVLPSPTNDGSLSVAILQSEHM 423

RESULT 10
ADO70389
ID ADO70389 standard; protein; 433 AA.
XX
AC ADO70389;
XX
DT 12-AUG-2004 (first entry)
XX
DE Unidentified plant transferase #3.
XX
KW plant; transferase; ACT; antimicrobial; pathogen resistance; enzyme;
KW agmatine coumaroyltransferase.
XX
OS Viridiplantae.
XX
PN WO2004044195-A2.
XX
PD 27-MAY-2004.
XX
PF 11-NOV-2003; 2003WO-EP012601.
XX
PR 12-NOV-2002; 2002EP-00025076.
XX
PA (RISO-) RISO NAT LAB.
XX
PI Rasmussem S, Burhenne K, Kristensen B;
XX
DR WPI; 2004-431667/40.
XX
PT New polynucleotide encoding a polypeptide having agmatine
PT coumaroyltransferase (ACT) activity, useful for establishing or enhancing
PT a pathogen resistance in a plant, and for producing a biopolymer.
XX
PS Disclosure; Fig 6; ilpp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC barley agmatine coumaroyltransferase (ACT) enzyme. The sequences are
CC useful for the preparation of an antimicrobial compound, its precursor or
CC a plant protection composition, for establishing or enhancing a pathogen
CC resistance in a plant, and for producing a biopolymer. The present
CC sequence is a transferase sequence used in a homology comparison with the
CC sequence of the invention.
XX
SQ Sequence 433 AA;

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Query Match 7.3%; Score 170.5; DB 8; Length 433;
Best Local Similarity 23.4%; Pred. No. 6e-07;
Matches 107; Conservative 61; Mismatches 153; Indels 137; Gaps 25;

QY 36 PTIVSTF--EQLGKR-FSEA-VPW--VAGQVKAEG-----ISEGNTGTSTFIVPFDPVPRV 84
Db 44 PTGASNFFPPQVMEKALSALVPFPYPMAGRLKRDGRIEIDCNGAGVLFVV--ADTPSV 101
QY 85 VVKDLRDD--PSAPTIEGMRKAGYPMAMFDEIIAPRKTL-IPGCTGPDPPKPVILLQL 141
Db 102 I-----DDGDFAPTL-----NL-----QLIPEVDHSTGIHS-FPLLVLQV 137
QY 142 NFIK-GGLILTVNGQHGAMVQGDVIRLLSKACRNDPTEBEMTAMNLDKRTIIVPYLE 200
Db 138 TPFKCGASLGVGMQHAADGFGSLHFINTWSDMAR-----GLD----- 176
QY 201 NYTIGEVHDIQVKA-----DVAGDAVLTPVSASWAFTEFSPKAM 241
Db 177 -LTIPFIDRTLRLARDPPQAFHVEYQAPSMKIPLDPSKSGPENTTVSIFKLTRDQL 235
QY 242 SELKDAATKTLDASTKFSVSTDDALSAFIWKASRVLELIDGSAPEFCRAVDA-----RP 297
Db 236 VALK--AKSKEDGNTVSYSSYEMLAGHVRSVGKAR--GLPNDQETKLYIATDGRSLRP 291
QY 298 AMGVSNNYPGLLQNTYHNSTI-----GEIANESLGATASRLRSELDPAS 342
Db 292 QLP-----PGYFGNVIFTATPLAVAGDLLSKPTWYAAGQIHDFLVRMDNLYLSALD--- 343
QY 343 MRQRTGLATYLNHNPDKNSVLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRR 402
Db 344 -----YLEMQPDLGALVRGAHTYKCPNLGITSWVRLPIYDADFQWG-----R 385
QY 403 PIPE-----PVESLMYFMPKPK-DGEFCAALSRLRDEDM 434
Db 386 PIFMGPGGIPYEGLSFVLPSPTNDGSLSVAILQSEHM 423

RESULT 11
ABU58179
ID ABU58179 standard; protein; 436 AA.
XX
AC ABU58179;
XX
DT 14-APR-2003 (first entry)
XX
DE Wheat stress response protein #7.
XX
KW Plant; EST; expressed sequence tag; stress response; drought; heat;
KW radiation; pathogen attack; grain flavour; disease resistance;
KW peptide-methionine sulphoxide reductase; DNA repair; enzyme;
KW intracellular protein transport.
XX
OS Triticum aestivum.
XX
PN US2002152497-A1.
XX
PD 17-OCT-2002.
XX
PF 19-FEB-2002; 2002US-00078929.
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PR 07-MAY-1999; 99US-0133038P.
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PA (FAMO/) FAMODU O O.
PA (MEYE/) MEYERS B C.

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Query Match 7.3%; Score 170.5; DB 3; Length 450;

Best Local Similarity 23.4%; Pred. No. 6.4e-07;

Matches 107; Conservative 61; Mismatches 153; Indels 137; Gaps 25;

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Db 61 PTGASNFDPQVMKALKALVFFYPMAGLKRDDGRIDEICNGAGVLFW--ADTPSV 118

QY 85 VVKDLRDD--PSAPTIEGKRGKAGYPMAMFENIIAPRKTLF-IGPGTGPDDPKPVILLQL 141

Db 119 I-----DDEGDFAPTL-----NL---RLIPEVDHSTGIHS-FPLLVLQV 154

QY 142 NFIK-GGLILTVNGQHGAMDMVQDAVIRLLSKACRNDPFTBEETAMNLDRTIIVPYLE 200

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Db      194  -LTIPFIDRTLRLARDPPQAFHVEYQAPSPMKIPLDPSKSGPENTTVSIFKLTRDQL 252
Qy      242  SELKDAATYTLDASTKFVSTDALSAPFIWKSASRVRLERIDGSAPEFCRAVDA---RP 297
Db      253  VALK--AKSKEDGNTVSYSYEMLAGHVWRSVGKAR--GLPNDQETKLYIATDGRSLRP 308
Qy      298  AMGVSNNYPGLLQNMTHNSTI-----GEIANESLGCATASRLRSLEDPAS 342
Db      309  QLP-----PGYFGNVIFTATPLAVAGDLLSKPTWYAAGQIHDFLVRMDNDYLSALD--- 360
Qy      343  MRQTRGLATYLNHNPKSNVSLTADPSTSVMLSSWAKVGLWYDFGLGKPKETVWR 402
Db      361  -----YLEMQPDLGALVRGATYKCPNLGITSWVRLPIYDADFQWG-----R 402
Qy      403  PIPE-----PVESLMYFMPKKP-DGEFCAALSRLDEDM 434
Db      403  PIFMFGGIPYEGLSVLPSPNTDGSLSVAIALQSEHM 440

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ID      AAG48446 standard; protein; 424 AA.
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AC      AAG48446;
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DT      18-OCT-2000 (first entry)
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DE      Arabidopsis thaliana protein fragment SEQ ID NO: 61177.
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KW      Protein identification; signal transduction pathway; metabolic pathway;
KW      hybridisation assay; genetic mapping; gene expression control; promoter;
KW      termination sequence.
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OS      Arabidopsis thaliana.
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PN      EF1033405-A2.
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PD      06-SEP-2000.
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PF      25-FEB-2000; 2000EP-00301439.
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Query Match 7.3%; Score 169.5; DB 3; Length 424;
Best Local Similarity 23.0%; Pred. No. 7.2e-07;
Matches 105; Conservative 61; Mismatches 156; Indels 135; Gaps 23;

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QY 85 VVKDLRDD--PSAPTIEGMRKAGYPMAMFENIAPRKTLPIGPGTGPDDPKVILLQLN 142
DB 93 I-----DDFGDFAPTL-----NL---RQLIPEVDHSGAHSFPLLVQVT 129
QY 143 FTK--GGLIITVNGOHGAMDVMGODAVIRLLSKACRNDPFTTEBMTAMNLDKRTIVPYLEN 201
DB 130 FFKCGGASLGVGMQHHADGFGSLHFINTWSDMAR-----GLD----- 167
QY 202 YTIIGPEVDHQIVKA-----DVAGGDAVLTPVSASWAFFTFSKAMS 242
DB 168 LTIPPFIDTLRLARPPQAPFHHVEYQAPSMKIPLDPSKGPENTVTSIFKLTQDLV 227
QY 243 ELKDAATKTLDASTKFSVTDALSAPFWKSASRVLERIDGSAPTFCRAVDA---RPA 298
DB 228 ALK--AKSKEDGNTVSYSYEMLAGHVRSVGKAR--GLPNDQETKLYATDGRSLRPQ 283
QY 299 MGVSNNYPGLLQNMTHNSTI-----GEIANESLGGATASRLRSELDPASM 343
DB 284 LP-----PGYFGNVIFTATPLAVAGDLLSKPTWYAAGQIHDFLVRMDDNLYRSALD--- 334
QY 344 RORTGLATYLNHNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPEVRRP 403
DB 335 -----YLEMQPDLSSALVRGAHTYKCPNLGITSWVRLPIYDADFGWG-----RP 377
QY 404 IFE-----PVESLMVFMPKKP--DGEFCAALSRLRDEDM 434
DB 378 IFWPGGIPYEGLSFVLPSPTNDGSLSAIALQSEHM 414

RESULT 14
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XX AAG48445;
AC AAG48445;
XX
DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 61176.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
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PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
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PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
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PR 12-OCT-1999; 99US-0158369P.

us-10-614-954-6.rag

Wed Jan 26 11:53:58 2005

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Search completed: January 23, 2005, 19:47:10
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 23, 2005, 16:28:15 ; Search time 817 Seconds
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Searched: 4300275 seqs, 2872944193 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1356	100.0	1356	13	US-10-614-954-5
3	915.6	67.5	1403	13	US-10-074-279-1
4	915.6	67.5	1403	16	US-10-614-954-1
5	915.6	67.5	12949	13	US-10-074-279-11
6	915.6	67.5	12949	16	US-10-614-954-11
7	915.6	67.5	13737	13	US-10-074-279-10
8	915.6	67.5	13737	16	US-10-614-954-10
9	249.8	18.4	1425	13	US-10-074-279-7
10	249.8	18.4	1425	16	US-10-614-954-7
11	146.2	10.8	695	18	US-10-653-047-4594
12	39.2	2.9	1947	15	US-10-369-493-27681

13	36.4	2.7	688	17	US-10-767-701-11710	Sequence 11710, A
14	36.2	2.7	684	17	US-10-767-701-11709	Sequence 11709, A
15	36	2.7	1707	18	US-10-425-115-66302	Sequence 66302, A
C 16	35.8	2.6	2463	16	US-10-320-797-7	Sequence 7, Appl
C 17	35.6	2.6	1459	18	US-10-363-345A-20283	Sequence 20283, A
C 18	35.6	2.6	1459	18	US-10-363-345A-20284	Sequence 20284, A
C 19	35.6	2.6	1463	18	US-10-363-345A-1033	Sequence 1033, Ap
C 20	35.6	2.6	1463	18	US-10-363-345A-1034	Sequence 1034, Ap
21	35.4	2.6	520	17	US-10-767-701-24625	Sequence 24625, A
22	35.4	2.6	2400	15	US-10-369-493-37751	Sequence 37751, A
23	35.2	2.6	801	17	US-10-437-963-84244	Sequence 84244, A
C 24	35.2	2.6	837	14	US-10-184-634-352	Sequence 352, App
C 25	35.2	2.6	837	14	US-10-184-634-352	Sequence 352, App
C 26	35	2.6	556	14	US-10-184-634-136	Sequence 136, App
C 27	35	2.6	556	14	US-10-184-634-136	Sequence 136, App
C 28	35	2.6	556	15	US-10-063-685-24	Sequence 24, Appl
C 29	35	2.6	2448	17	US-10-437-963-86614	Sequence 86614, A
30	34.6	2.6	427	16	US-10-374-780A-932	Sequence 932, App
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32	34.6	2.6	1112	13	US-10-027-632-31187	Sequence 31187, A
33	34.6	2.6	1112	13	US-10-027-632-31188	Sequence 31188, A
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C 36	34.2	2.5	1377	15	US-10-369-493-46533	Sequence 46533, A
C 37	34	2.5	1584	16	US-10-282-122A-27075	Sequence 27075, A
38	34	2.5	1770	18	US-10-411-910A-110	Sequence 110, App
C 39	34	2.5	3115	18	US-10-363-345A-30243	Sequence 30243, A
40	34	2.5	3115	18	US-10-363-345A-30244	Sequence 30244, A
41	34	2.5	269223	16	US-10-672-787-41	Sequence 41, Appl
42	33.8	2.5	322	16	US-10-242-535A-19650	Sequence 19650, A
43	33.8	2.5	322	16	US-10-085-783A-19650	Sequence 19650, A
C 44	33.8	2.5	549	18	US-10-425-115-111874	Sequence 111874, A
45	33.8	2.5	2913	15	US-10-172-118-442	Sequence 442, App

ALIGNMENTS

RESULT 1

US-10-074-279-5 -
; Sequence 5, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Fusarium graminearum
US-10-074-279-5

Query Match	100.0%	Score 1356	DB 13	Length 1356
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1356	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	ATGGCTTTCAAGATACAGCTCGACACCCCTCGGCGAGCTACCGGCTCTCTTCGATCTAC	60	
Db	1	ATGGCTTTCAAGATACAGCTCGACACCCCTCGGCGAGCTACCGGCTCTCTTCGATCTAC	60	
QY	61	ACCAAAATCAGTCTCTCTTACCCCGCTCTGTGATTCCTCTCAATATCCACTATTGTGAGC	120	

421 CTCAACTTCATCAAGGGCGGACTCATCTCCTCAGTGTCAACGGACAGACCGGTGCTATGGAT 480
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481 ATGGTAGGCAAGATCGGTGATCGGTCTACTCTCAAGCGGTGCGTAACGACCCATTTC 540
Db ATGGTAGGCAAGATCGGTGATCGGTCTACTCTCAAGCGGTGCGTAACGACCCATTTC 540
481 ACCGAAGAGAAATGATCGGCCATGAACCTCGATPCGCAAGACGATAGTCTTACCTTGAA 600
Db ACCGAAGAGAAATGATCGGCCATGAACCTCGATPCGCAAGACGATAGTCTTACCTTGAA 600
601 AACTATACGATGGCCCCCGAGGTAGATCATCAGATTGTCAAGCTGATGTAGCTGTGTGT 660
Db AACTATACGATGGCCCCCGAGGTAGATCATCAGATTGTCAAGCTGATGTAGCTGTGTGT 660
661 GACGCTGTTCTCAGCGCGGTGAGTCAAGCTGGCGGTCTTCAATTCAGCCCAAGGCC 720
Db GACGCTGTTCTCAGCGCGGTGAGTCAAGCTGGCGGTCTTCAATTCAGCCCAAGGCC 720
721 ATGTCAAGCTCAAGGATGCTGTACCAAGACTCTTGACGCATCAACAAAGTTCTGTGTCG 780
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781 ACTGACGATGCTCTTTCGGGGTTCATCTGGAATCGGCCTCTCGCGTGCCTCGGAAGA 840
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841 ATCGATGGCTCTGACCTACCGAGTTCTGCGGTGCTGTTGATGCTCGACCGGCAATGGGT 900
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901 GTCTCGAAACAACCTACCGAGCTTCTTCAAAACATGACCTTACCAACCTCGACCATCGGC 960
Db GTCTCGAAACAACCTACCGAGCTTCTTCAAAACATGACCTTACCAACCTCGACCATCGGC 960
961 GAAATCGCAACGAGTCACTCGCGGCAACAGATCAAGCTTGGTTTCAAGACTCGACCCC 1020
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1141 GCCAAGTGGGACTCTGGGATTAACGATTTGGGCTCGGACCTTACGAGCTCATGCTGAGTTG 1200
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1261 GCGAGTCTTGTGCGCGCTTCTCTGAGGAGTATGAGGATATGACCGATTGAAGGCGGAT 1320
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RESULT 3

US-10-074-279-1
; Sequence 1, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.

; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Fusarium sporotrichioides
; US-10-074-279-1

Query Match 67.5%; Score 915.6; DB 13; Length 1403;

Best Local Similarity 80.3%; Pred. No. 2.6e-306;

Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

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Db 96 CCAGATCAGTCTCGTTTACCCGCTCTCTGATCCCTCCAGTATCCCACTATCTGTCAGCAC 155
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QY 183 AGCGAGGACATTTAGCGGAGAAACACAGAACTCTCTTTATCGTCCCTTTTCAGGACGT 242
Db 216 GACCGAGGACATCGCGAAGAAACACAGAACTCTCAAGATCATTTCAATGAGGAGAC 275
QY 243 TCCTCGTGTGTAGTGAAGACCTCGCGATGATCTTCAGCGCCCAACGATCGAGGGTAT 302
Db 276 ACCCGCTCTTGTGTGAAGACCTCGTGTATCTCTCAGCGCCCAACGATCGAGGGTT 335
QY 303 GAGAAAGCGGATACCTTATGGGATGTTTACAGGAACATCATCGGCCAAGGAAGAC 362
Db 336 GAGAAAGCGGTTTCCCTTAGAGATGTTTACAGGAACGCTCGTCTCCGAGGAAGAC 395
QY 363 GTTACCTATTGACCTTGTGCTCCGACCAACCAAGCCTGTAATTTCTATTGACGCT 422
Db 396 ATTAGCTATCGGACCTTGGCAATGGCCCAACGACCCGAGCCTGTGTTGCTATTGAGCT 455
QY 423 CAACTTCATCAAGGGCGGACTCATCTCCTCACTGTCAACGGACAGACGGTGTATGGATAT 482
Db 456 CAACTTCATTAAGGGCGGACTCATCTCACCCTCAACGGACAACTGTTGCTATGGACAT 515
QY 483 GGTAGCCCAAGATGCGGTGATCGGTCTACTCTCAAGGGGTGCGGTAAAGACCCATTAC 542
Db 516 GACAGGACCAAGATGCAATTTATTCGTCTTCTTCCAAAGGGTGGCCCAACGAATCATTTAC 575
QY 543 CGAAGAGGAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTTCTTACCTTGAAGA 602
Db 576 CGAGGAGGAATGCTCGGCCATGAACCTCGATCGCAAGCGGTAGTCCCTCTCTCTTGAAGA 635
QY 603 CTATACGATTGGCCCCCGAGGTAGATCATCAGATTGTCAAGCTGTATGTAGCTGGTGTGA 662
Db 636 CTACAAAGTTGGTCTCTGAGCTAGACCAACGATCGCAAAACC--TGCCTCTGCTGGCGA 692
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QY 723 GTCAGAGCTCAAGGATGCTGTACCAAGACTCTTGAACGATCAACAAAGTTCTGTGTGAC 782
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1263 CGAGTTCTGTGGCGCTTTCTCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 1322
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1293 GAGTTTACGGCGTCAATTTCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 1352
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1323 GGAGTGGACCAAGTATGCGAGTACGTTGGTTAG 1356
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RESULT 4

US-10-614-954-1
; Sequence 1, Application US/10614954
; Publication No. US20040034884A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmemon, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/614,954
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Fusarium sporotrichioides
US-10-614-954-1

Query Match 67.5%; Score 915.6; DB 16; Length 1403;
Best Local Similarity 80.3%; Pred. No. 2.6e-306;
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

Qy 3 GCCTTTCAGATACAGCTCGACACCTCGCGCAGCTACCGGCTCTTTCGATCTACAC 62

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36 GTCTTTGACATAGAGCTCGACATCATCGGCAGCAACCGCTCTTCTTCAATCTACAC 95
Qy
63 CCNAATCACTCTCTCTACCCGCTCTCTGATTCCTCTCAATATCCCACTATTTGTGAGCAC 122
Db
96 CCAGATCACTCTCTGTTTACCCGCTCTCTGATCCCTCCAGTATCCCACTATCGTTCAGCAC 155
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396 ATTAGCTATCGACCTTGGCAATGGCCCAACAGCCGAGCCTGTGTTGCTATTCAGCT 455
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456 CAACTTCATCAAGGCGGACTCATCTCACTCTCAAGGCGTGGCGCAACGAATCATTCAC 515
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576 CGAGGAGGAATCTCGGCCATGAACCTCGATCGAAGACGATGTCCTCTCTCTTGAAGAA 635
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603 CTATACGATTTGGCCCGAGGTAGATCATCAGATTTGTCAAAGCTGATGATGCTGGTCTGA 662
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663 CGCTGTTCTCACGCGGTGAGTCAAGCTGGCGTTTCTTCAATTCAGCCCCCAAGSCCAT 722
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693 CGCTCCACCGCAACCGGCAAGGCTGGCGTTTCTTTCATTCATTCCTCCCAAGSCCT 752
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783 TGACGATGCTCTTTCGCGGTTCATCTGGAATTCGCGCTCTCGCGTGGCTCTCGAAGAAAT 842
Db
813 TGATGATGCTCTTTCGCGGTTCATCTGGAATTCGCGCTCTCGCGTGGCTCTCGAAGAAAT 872
Qy
843 CGATGGCTCTGACCTACCGAGTTCCTGCGGTGCTGTGATGCTCGACCGGCAATGGGTGT 902
Db
873 GGATGCTTCCACCTACTGAAATCTGCGCGCTGTCGACATGCGGGGCCCAATGGGCGT 932
Qy
903 CTCGAACTACCTACCGGCTTCTTCAAAACATGACTTACCACTACCACTCGACCATCGGCGA 962
Db
933 ATCAAGCATATACCGAGGCTCTTTCAAAAACATGACTTACCACTACCACTCGACCGTCCCGA 992
Qy
963 AATCGCCCAAGCTCACTCGCGGCAACAGCATCACGCTTCTGTTTCAAGAACTCGACCCCGC 1022
Db
993 AATCGCCCAAGCTCACTTGGCGCAACAGCATCACGCTGCTCGGACTCAACAGTGA 1052
Qy
1023 GAGCATGCGCCAGCAACAAGAGGTCTCGCAGCTACTCTGCAACAACACCCCGCAAGTTC 1082
Db
1053 TCGTTTGGCAGACGAAACAAAGCTTTTGGCGAGCTACATGATGCTGCTGCTGCAAGTTC 1112
Qy
1083 CAACTGATCCCTGAGGCTGATGCGGACCCATCTACCGGCTCATGCTGAGTTCTTGGGC 1142

Db	1113	GAGGCTCTCCCTGACCGCCGATCGGAATCCGTCAAGCAGCATCATGCTGATGTCCTGGGC	1172
Qy	1143	CAAGTGGGACTCTGGGATTAACGACTTTGGGCTCGGACTGGGTAAGCCCGAGACTGTGAG	1202
Db	1173	CAAGTGGGATGCTGGGAGTATGACTTTGGGTTGGACTGGGTAAGCCTGAGAGTGTGAG	1232
Qy	1203	ACGGCCAACTTTGAGGCTGTTGAGAGCTTGTGATGTTACTTTATGCCCAAGAGCCTGATGG	1262
Db	1233	AAGACCTCGCTTTGAACCTTTTGGAGGTTTGTATGTACTTTATGCCCAAGAGCCTGATGG	1292
Qy	1263	CGAGTTCTGTGCGGCGCTTCTCTGAGGATGAGGATATGACCGGATTGAAGCGGATAA	1322
Db	1293	GGAGTTTACGGCTTCATTTCTGAGGATGAGGATATGAGAGACTAAAGCGGATGA	1352
Qy	1323	GGAGTGGACCAAGTATCGCAGTACGTTGGTTAG	1356
Db	1353	GGAGTGGACCAAGTACGCAAGTATATTGGGTAG	1386
RESULT 5			
US-10-074-279-11			
; Sequence 11, Application US/10074279			
; Publication No. US20020162136A1			
; GENERAL INFORMATION:			
; APPLICANT: Hohn, T.			
; APPLICANT: Salmeron, J.			
; APPLICANT: Peters, C.			
; APPLICANT: Kendra, D.			
; APPLICANT: Reinders, J.			
; APPLICANT: Kuznia, R.			
; APPLICANT: Dill-Mackey, R.			
; TITLE OF INVENTION: Transgenic Plant and Methods			
; FILE REFERENCE: sequence list			
; CURRENT APPLICATION NUMBER: US/10/074,279			
; CURRENT FILING DATE: 2002-02-12			
; PRIOR APPLICATION NUMBER: US/09/538,414			
; PRIOR FILING DATE: 2000-03-29			
; NUMBER OF SEQ ID NOS: 11			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 11			
; LENGTH: 12949			
; TYPE: DNA			
; ORGANISM: Plasmid			
US-10-074-279-11			
Query Match			
Best Local Similarity 67.5%; Score 915.6; DB 13; Length 12949;			
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;			
Qy	3	GGCTTTCAAGATACAGCTCGACACCCCTCGGCCAGCTACCAGGCTCTCTTTTCGATCTACAC	62
Db	11281	GTCTTTGACATAGAGCTCGACATCATCGCCAGCAACCGCTCTCTTTCAATCTACAC	11340
Qy	63	CCMAATCAGTCTCTTACCCGCTCTGATTCCTCTCAATATCCCACTATTGTGAGCAC	122
Db	11341	CCAGATCAGTCTCGTTTACCCGCTCTGATCCCTCCAGATATCCCAACCATCGTCAGCAC	11400
Qy	123	CTTTCGAGCAAGTCTTAAAGCGCTTCTCCGAAGCGTCCCATGGTCGCGAGCCAGGTCAA	182
Db	11401	CCTTGAGGAAGGCTTAAAGCGCTCTCTCAACCTTCCCATGGTTCGCGGCCAGGTCAA	11460
Qy	183	AGCCGAGGCGATTAGCGAGGAAACACAGGAACTCTCTTTATCGTCCCTTTTTCGAGGACGT	242
Db	11461	GACCGAGGCGCATCAGCGAAGGAACACAGGAACTCTCAAGATCATTTCCATATGAGGAGAC	11520
Qy	243	TGCTGTGTGTAGTGAAGACCTCGCGATGATTCCTTTCGAGGCGCCACCATCGAGGGTAT	302
Db	11521	ACCCCGTCTGTGGTGAAGACCTCGGTGATGATTCCTCAGCGCCCAACCATCGAGGGGTT	11580
Qy	303	GAGAAAGCGGCGATACCTTATCGCATGTTTCAGAGAACATCATCGCCCGAGGAGAC	362
Db	11581	GAGAAAGCGGCGGTTTCCCTTAGATGTTTTCAGAGAACATCGTCTCGCTCCGAGGAAGAC	11640

RESULT 6
US-10-614-954-11
; Sequence 11, Application US/10614954
; Publication No. US20040034884A1

Qy	363	GTTAACCTATTGGACCTGGTACTGGTCCCGACGACCCAAAGCCCTGTAAATCTATTGACGCT	422
Db	11641	ATTAGCTATCGGACCTGGCAATGGCCCAACGACCCGAGCCTGTGTGTTATTGACGCT	11700
Qy	423	CAACTTCATCAGGGCGGACTCATCTCACTGTCAACGAGACGACGGTCTATGGATAT	482
Db	11701	CAACTTCATTAAGGGCGGACTCATCTCACCGTCAACGGAACAACATGGTGTATGGACAT	11760
Qy	483	GGTAGGCCAAGATGCGGTGATCCGTCTACTCTCAAGGGGTGCCGTAAACGACCATTCAC	542
Db	11761	GCAGAGCAAGATGCAATTTATTCGTCTTCTCCTCAAGGGGTGCCGCAACGATCATTCAC	11820
Qy	543	CGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCTTTCATCTTGAATA	602
Db	11821	CGAGGAGGAAATCTCGGCCATGAACCTCGATCGCAAGACGATAGTTCTTCTCCTTGAATA	11880
Qy	603	CTATACGATTTGCCCGGAGGTAGATCATCAGATTGTCAAGCTGTAGTCTGTTGGTGA	662
Db	11881	CTACAAAGTTGGTCTGAGCTAGACCACGATCGCCAAACC--TGCGCTCTCTGGCGA	11937
Qy	663	CGCTGTTCTCAAGCCGCTCAGTGCAAGCTGGGGCTTCTTTCACATTCAGCCCAAGGCCAT	722
Db	11938	CGCTCCACCGCACCGGCCAAGGCAAGCTGGGGCTTCTTTCATTCATCTCCCAAGGCCCT	11997
Qy	723	GTGAGAGCTCAAGGATGCTGCTACCAAGACTCTTGACGATCAACAAAGTTCTGTGTCGAC	782
Db	11998	CTCGGAGCTGAAAGACGCGACCAAGAACTCTTGACGGCTCTGCAAGTTTGTGTCAAC	12057
Qy	783	TGACGATGCTCTTTGGCGCTTCTGGAATTCGGCTCTCGCGTGGCTCTCGAAAGAT	842
Db	12058	TGATGATGCTCTTTGGCGCTTCTTTCGCAATCAACCTCGCGCTACGCTCTCCCAAGAT	12117
Qy	843	CGATGCTCTGCAACCTTACCGAGTTCTGCGCTGTGTGTGATGCTCGACCGGCAATGGTGT	902
Db	12118	GSATGCTTCCACACTACTGAAATTCGCGCGCTGTGACATCGGGGGCCCAATGGCGCT	12177
Qy	903	CTCGAAACTACCCAGGCTTCTTCAAAACATGACCTACCAACACTCGACCAATCGGCGA	962
Db	12178	ATCAAGCATATACCCAGGCTTCTTCAAAACATGACCTACCAACACTCGACCGTCCCGA	12237
Qy	963	AATCGCCACGAGTCACTCGGCGCAACAGCATCAGCCCTTCTGATGAGAACTCGACCCGCG	1022
Db	12238	AATCGCCAAACGAAACCACTTGGCGCAACAGCATCAGCCCTCGCGCTCGGAACTCAACAGTGA	12297
Qy	1023	GAGCATGCGCCACGAAACAAAGAGGCTCTCGCGAGTCTCGGACGTAACCAACAAACCCGACAAAGTC	1082
Db	12298	TGCTTTGCGCACGACGAAACAAAGCTTTGCGGAGTACATGCTGCTGCTGACAAAGTC	12357
Qy	1083	CAAGCTATCCCTGACGGCTGATCGGACCCATCTTACAGCGTCACTGCTGAGTTCTTGGGC	1142
Db	12358	GAGCGTCTCCCTGACCGCGATGCGAATCCGTCAGCAGCATCATGCTGAGTTCTTGGGC	12417
Qy	1143	CAAGTGGGACTCTGGGATTACGCTTTGGGCTCGGACTGGGTAAAGCCCGAGACTGTGAG	1202
Db	12418	CAAGTGGGATGCTGGGATGATGACTTTGGGTTTGGACTGGGTAAAGCCCTGAGAGTGTGAG	12477
Qy	1203	ACGGCCAAATCTTTGAGCGCTGTTGAGAGCTTGTATCTTTATGCCCAAGAGCTCATGG	1562
Db	12478	AAGACTCGCTTTGAACCTTTTGAAGTTTGAAGTTTGAATCTTTATGCCCAAGAGCTCATGG	12537
Qy	1263	CGAGTTCTGTGCGGCTTTCTCTGAGGATGAGGATATGGACCGATTGAAGCGGATAA	1322
Db	12538	GGAGTTTACGGGCTCCATTTCTCTGAGGATGAGGATATGGAGAGACTAAAGCGGATGA	12597
Qy	1323	GGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG	1356
Db	12598	GGAGTGGACCAAGTATGCGCAGTATATTGGGTAG	12631

GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/614,954
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 12949
; TYPE: DNA
; ORGANISM: Plasmid
US-10-614-954-11

Query Match 67.5%; Score 915.6; DB 16; Length 12949;
Best Local Similarity 80.3%; Pred. No. 8.1e-306;
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

QY	3	GGCTTTCAAGATACAGCTCGACACCTCGCGCAGCTACCAGGCTCTCTTTTCATCTACAC	62
DB	11281	GTCTTTTGACATAGAGCTGCATCATCGCCAGAACCGCTCTCTTTCAATCTACAC	11340
QY	63	CCAAATCAGTCTCTCTACCCCGTCTCTGATCTCTCAATATCCCACTATTGTTCAGCAC	122
DB	11341	CCAGATCAGTCTGTTTACCCCGTCTCTGATCTCTCCAGTATCCCACTATGTCAGCAC	11400
QY	123	CTTCGAGCAAGGTCTTAAGCGCTTCTCCGAGCGCTCCCATGGTCCGAGGCCAGGTCAA	182
DB	11401	CCTTGAGGAAGGCTTAAACCGCTCTCTCAAACTTCCCATGGTCCGCGCCAGGTCAA	11460
QY	183	AGCCGAGGCGATTAGCGAGGGAACACAGAACTCTCTTTATCGTCCCTTTTGGAGCGT	242
DB	11461	GACCGAGGCGATCAGCGAAGGAACACAGAACTTCCAGATCATTCATATGAGGAGAC	11520
QY	243	TCCTCGTGTGTAGTGAAGACCTCCGCGATGATCTTTCAGCGCCACCGATCGAGGGTAT	302
DB	11521	ACCCGCTCTTGTGTGAAGACCTCCGCGATGATCTTCTCAGCGCCAAACGATCGAGGGTT	11580
QY	303	GAGAAAGCGGGATACCTTATGCGATGTTTGAAGAAATCATCTCGCGCCAGGAGAC	362
DB	11581	GAGAAAGCGGGTTTCCCTTATGAGATGTTTGAAGAAATGTTTGAAGAAATGTTTGAAGAA	11640
QY	363	GTTTACCTATTGGACCTGGTACTCGTCCGAGACCCAAAGCCCTGTAAATCTATTGCGCT	422
DB	11641	ATTAGCTATCGGACCTGGCATGGTCCGCGCCAAAGCCCTGTGTGCTATTGCGCT	11700
QY	423	CAACTTCATCAAGGCGGACTCATCTCTCACTGTCAACGGACAGACCGGTGCTATGATAT	482
DB	11701	CAACTTCATTAAAGGCGGACTCATCTCTCACTGTCAACGGACAGACCGGTGCTATGATAT	11760
QY	483	GGTAGGCAAGATCGCGTGTATCGTCTACTCTCAAGGCGTCCGTAACGACCCATTAC	542
DB	11761	GACAGGCAAGATGCAATTTATCTCTCTCTCAAGGCGTCCGTAACGACCCATTAC	11820
QY	543	CGAAGAGGAATCAGCGCCATGAACCTCGATCCGAGACGATAGTTCCTTACCTTCAAAA	602
DB	11821	CGAGGAGGAATCTCGGCCATGAACCTCGATCCGAGACGATAGTTCCTTCTTCAAAA	11880
QY	603	CTATACGATTGGCCCGAGGTAGATCATCATGATTGTCAAGCTGATGTAGCTGGTGTGA	662
DB	11881	CTACAAAGTTGGTCTTGAAGTACGATCATCATGATTGTCAAGCTGATGTAGCTGGTGTGA	11937
QY	663	CGCTGTCTCAGCGCGTGTAGTCAAGCTGGCGTCTTCAATTCAGTTCAGCCCGGCGCAT	722
DB	11938	CGTCCACCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	11997

RESULT 7

US-10-074-279-10
; Sequence 10, Application US/10074279
; Publication NO. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 13737
; TYPE: DNA
; ORGANISM: Plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
US-10-074-279-10

Query Match		67.5%;	Score 915.6;	DB 13;	Length 13737;
Best Local Similarity		80.3%;	Pred. No. 8.4e-306;		
Matches 1087;		Conservative	0;	Mismatches 264;	Indels 3; Gaps 1;
Qy	3	GGCTTCAAGATACAGCTCGACACCTCGCGCAGCTTACAGGCTTCTTTCGATCTACAC	62		
Db	50	GTCTTTTGACATAGAGCTCGACATCATCGCGCAGCAACCGCTCTTCTTTCATCTACAC	109		
Qy	63	CCAAATCAGTCTCTTACCCGCTCTCTGATCTCTCAATATCCACATATTTGTGAGAC	122		
Db	110	CCAGATCAGTCTGTTTACCCGCTCTCTGATCCCTCCAGTATCCACCATCGTCAGAC	169		
Qy	123	CTTCGAGCAAGGCTTTAAGCGTTTCCGAAGCGTCCCATGGTGCAGGCGAAGTCAA	182		
Db	170	CCTTGAGGAAGGCTTAAAGCGCTCTCTCAAACCTTCCCATGGTGCAGGCGAGTCAA	229		
Qy	183	AGCCGAGGCGATAGGAGGGAACACAGGAATCTCTTTATCGTCCCTTTTGAGGAGCT	242		
Db	230	GACCGAGGCGATCAGCGAAGGAACACAGGAATCTTCCAAAGTCAATTCATATGAGGAG	289		
Qy	243	TCCTCGTGTGTAGTGAAGACCTCGCGATGATCTTCCAGCGCCACCATCGAGGAT	302		
Db	290	ACCCGCTTGTGTGAAGACCTCGTGTATGATCTCTCAGGCGCAACGATCGAGGGTT	349		
Qy	303	GAGAAAGCGGATACCTTATCGCGATGTTTGAAGGAACATCATCGCGCCCAAGGAAGAC	362		
Db	350	GAGAAAGCGGTTTCCCTTGAAGATGTTTGAAGGAACGTCGTCGCTCCGAGGAAGAC	409		
Qy	363	GTTACCTATTGACCTGTGTTACTGTTCCGACGACCCAAAGCCCTGTAAATCTATTGAGCT	422		
Db	410	ATTAGCTATCGGACCTGGCAATGGGCCCAACGACCCGAAAGCCGTGTGCTATTGCGAGT	469		
Qy	423	CAACTTTCATAGGGCGGACTATCTCTCACTGTCAACGACAGCAGCGTGTATGATAT	482		
Db	470	CAACTTTCATAGGGCGGACTATCTCTCACTGTCAACGACAGCAGCGTGTATGATAT	529		
Qy	483	GGTAGGCCAAGATCGGGTGTATCGGTCTACTCTCCAGGGCGTCCGTAACGCCCAATTCAC	542		
Db	530	GACAGGACAAGATGCAATTAATTTGCTCTCTCCAAAGCGTCCGCAACGAATCATTTAC	589		
Qy	543	CGAAGGGAATGACGGCCATGAACCTCGATCGCAAGAGATAGTTCCTTACTTTGAAAC	602		
Db	590	CGAGGAGGAATCTCGGCCATGAACCTCGATCGCAAGAGCGTATGCTCTCTCTTGAAC	649		
Qy	603	CTATACGTTGCCCGGAGTATCATCAGATTGTCAAAGCTGTAGTGTGTTGTCGA	662		
Db	650	CTACAAAGTTGGTCTGAGCTAGACCAACAGATCGCAACCC---TGGCCCTGTGGCGA	706		
Qy	663	CGCTGTTCTCAGCGCGTCAAGCTCGGCGTTCTTTCATTCAGGCCCAAGGCCAT	722		
Db	707	CGCTCCACCGCACCGGCCAAGCAAGCTGGGCGTTCTTTTCATTCACCTCCCAAGGCCCT	766		
Qy	723	GTACAGCTCAAGATGCTGTACCAAGACTCTTGACGATCAACAAAGTTGCTGTCGAC	782		
Db	767	CTCGAGCTGAAAGAGCGACGCCACAAAGACTCTTGACGGGTGTCGCAAGTTTGTGTCAC	826		
Qy	783	TGACGATGCTCTTTTGGCGGTTCTATCGGAATCGGCTCTCGCGTGCCTCGAAGAT	842		
Db	827	TGATGATGCTCTTTTGGCGGTTTATCGGAATCAACCTCGCGGTACGCTCTCGAAGAT	886		
Qy	843	CGATGCTCTGACCTTACCGAGTTCTGCGGTGCTGTGTGATGCTCGACCGGCAATGGGTG	902		
Db	887	GGATGCTTCCACACCTACTGAAATCTGCGCGCTGTGCGATCGCGGGGCCAATGGCGT	946		
Qy	903	CTCGAACAATACCCAGGCTTCTTCAAACATGACCTTACCAACATCGACCATCGGCGA	962		
Db	947	ATCAAGCATATACCCAGGCTTCTTCAAACATGACCTTACCATGATCGACCGCTCGCGCA	1006		
Qy	963	ATCGCCACGAGTACTCGGCGCACAGCATCAGCCCTTCTGTTAGAACTCGACCCCGC	1022		
Db	1007	AATCGCCACGAACCACTTTGGGCGCAACGATCAGCCCTCGCGCTCGGAATCAACAGTGA	1066		

RESULT 8
US-10-614-954-10
; Sequence 10, Application US/10614954
; Publication No. US20040034884A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/614,954
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 13737
; TYPE: DNA
; ORGANISM: Plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
US-10-614-954-10

Query Match		67.5%;	Score 915.6;	DB 16;	Length 13737;
Best Local Similarity		80.3%;	Pred. No. 8.4e-306;		
Matches 1087;		Conservative	0;	Mismatches 264;	Indels 3; Gaps 1;
Qy	3	GGCTTCAAGATACAGCTCGACACCTCGCGCAGCTTACAGGCTTCTTTCGATCTACAC	62		
Db	50	GTCTTTTGACATAGAGCTCGACATCATCGCGCAGCAACCGCTCTTCTTTCATCTACAC	109		
Qy	63	CCAAATCAGTCTCTTACCCGCTCTCTGATCTCTTCAATATCCACATATTTGTGAGAC	122		
Db	110	CCAGATCAGTCTCTTACCCGCTCTCTGATCCCTCCAGTATCCCAACCATCGTCAGAC	169		
Qy	123	CTTCGAGCAAGTCTTAAAGCGCTTCTCCGAAGCGTCCCATGGTGCAGGCGGAGTCAA	182		
Db	170	CCTTGAGGAAGGCTTAAAGCGCTCTCTCAAACCTTCCCATGGTGCAGGCGGAGTCAA	229		
Qy	183	AGCCGAGGCGATTAGCGAGGGAACACAGGAATCTCTTTATCGTCCCTTTTGAGGAGCT	242		
Db	230	GACCGAGGCGATCAGCGAAGGAACACAGGAATCTTCCAAAGTCAATTCATATGAGGAG	289		

243 TCCTCGTGTGTAGTAAGACCTCGCGATGATCTTTCAGCGCCACGATCGAGGTAT 302
Db |||||
290 ACCCGTCTTGTGTGAAGACCTCGTGATGATCTTTCAGCGCCAAAGATCGAGGGTT 349
Qy |||||
303 GAGAAAGCGGGATACCTATCGGATGTTTACAGAAACATCATCGCGCCAAAGAAC 362
Db |||||
350 GAGAAAGCGGGTTCCTTGAAGATGTTTACAGAAACATCGTGTCTCGCGAAAGAC 409
Qy |||||
363 GTTACTATTGACCTGTGTGCTCCGACGACCAAGACCTGTAAATCTATTTCAGCT 422
Db |||||
410 ATTAGCTATCGGACCTGGCAATGGCCCAAGCAAGCGAGCTGTGTCTATTGACGT 469
Qy |||||
423 CAACTTTCAATGAGGCGGACTCATCTCTCAACGACAGCAAGCGGTGTATGATAT 482
Db |||||
470 CAACTTTCAATGAGGCGGACTCATCTCAACGACAGCAAGCGGTGTATGATAT 529
Qy |||||
483 GTTAGCCAAAGATCGGCTGATCGGTCTACTCTCAAGGCGTCCGTAAGCCCAATTCAC 542
Db |||||
530 GACAGGACAAGATGCAATTTATTCGTCTCTCAAGGCGTCCGCAAGCAATTCAC 589
Qy |||||
543 CGAAGAGGAAATGACGGCCATGAACCTCGATCGAAGAGATAGTTCTTACCTTGAAA 602
Db |||||
590 CGAGAGGAAATCTCGGCCATGAACCTCGATCGAAGAGATAGTTCTTCTTGAAA 649
Qy |||||
603 CTATAGATTGGCCCGGAGTATCATCAGATTGTCAAAGCTGATGTAGTGGTGA 662
Db |||||
650 CTACAAAGTTGTTCTGCTAGCTAGACCAACAGATCGCAAAAC--TGCCTGTCTGGCA 706
Qy |||||
663 CGCTGTTCTACGCGGTCAGTGAAGCTGGGGTCTTTCATTCAGCCCAAGCCAT 722
Db |||||
707 CGCTCACCGCCAGCGCAAGCTAGCTGGGGTCTTTCATTCAGCTCCCAAGCCCT 766
Qy |||||
723 GTCAGAGCTCAAGGATGCTTACCAAGACTCTTGACGATCAAAAGCTGTGTGTCAG 782
Db |||||
767 CTCGGAGCTGAAGAGCGAGCCACAAGACTCTTGACGCTGTCCAAGTTGTGTCAAC 826
Qy |||||
783 TGAAGTGTCTTTTCGGCTTCATCTGGAATTCGGCTCTCGCGTGTCTCGAAGAAAT 842
Db |||||
827 TGATGATGCTCTTTTCGGCTTTATCTGGAATTCAGCTCGCGCTGTGCAAGATT 886
Qy |||||
843 CGATGCTCTGACCTTACGAGTTCGCGTCTGTGTGATGTCGACCGGCAATGGTCT 902
Db |||||
887 GGAATGCTTCCACACCTTACTGAATTCGCGCGCTGTGCAATGCGGGGCCAATGGGCT 946
Qy |||||
903 CTCGAACAACTACCAAGGCTCTTCAAAACATGACTTACCACAACTCGACCATCGGCA 962
Db |||||
947 ATCAAGCACAATACCAAGGCTCTTCAAAACATGACTTACCACAACTCGACCATCGGCA 1006
Qy |||||
963 AATCGCCAAAGTCACTCGCGCAACAGATCAAGCTTGTGTAAGTCAAGTCAAGCCCGC 1022
Db |||||
1007 AATCGCCAAAGTCACTCGCGCAACAGATCAAGCTTGTGTAAGTCAAGTCAAGCCCGC 1066
Qy |||||
1023 GAGCATGCGCCAGCAAGAGGTCTCGAGTACCTGCAACAAACCCGACAAAGTC 1082
Db |||||
1067 TCGTTTGGCGAGCAAGCAAGCTTGGCGAGTACATGATGCTGTGCAAGTCAAGTCA 1126
Qy |||||
1083 CAACTGATCTCTGACGCTGATCGGACCCATCTACAGCGTCAATGCTGAGTTCTTGGGC 1142
Db |||||
1127 GAGCGTCTCTTACGCGCGATCGAATCGTCAAGCAGCATCATGCTGAGTTCTTGGGC 1186
Qy |||||
1143 CAAAGTGGGACTCTGGGATTAAGCTTTGGGCTCGGACTGGGTAAAGCCGAGCTGTAG 1202
Db |||||
1187 CAAAGTGGGATGCTGGGATGATGACTTTGGGTTTGGACTGGGTAAAGCCCTGAGAGTGTAG 1246
Qy |||||
1203 ACGGCCAATCTTTGAGCTTTCAGAGCTTGTATGTTTATGCCCAAGAGCTCATGG 1262
Db |||||
1247 AAGACTCTGTTTGAACCTTTTGAAGTTTGTATCTTTATGCCCAAGAGCTGTAGTGG 1306
Qy |||||
1263 CGAGTTCTGTGCGCGCTTTCTCTGAGGATGAGGATATGAGCCGATTTGAAGCCGATAA 1322
Db |||||
1307 GGAGTTTACGCGCTTCATTTCTCTGAGGATGAGGATATGAGAGACTAAAGCCGATGA 1366
Qy |||||
1323 GGAGTGACCAAGTATGCGCAGTACGTTGGTTAG 1356

Db 1367 GGAGTGCAAAAGTACGCAAGATATATTGGGTAG 1400
RESULT 9
US-10-074-279-7
; Sequence 7, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/10/074,279
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-074-279-7
Query Match 18.4%; Score 249.8; DB 13; Length 1425;
Best Local Similarity 51.9%; Pred.No. 3.6e-75;
Matches 700; Conservative 0; Mismatches 622; Indels 27; Gaps 5;
Qy 16 CAGCTCGACACCTCGGCGAGCTACGAGCGCTCTTCGATCTACACCCAAATCAGTCTC 75
Db 64 CAACTGTATTTTGGGACACAACTTCGCTATACAAATACACTCAATATGCTCT 123
Qy 76 CTCTACCCCGTCTGTGATTCCTCAATATCCACTATTGTGACGACCTTCGAGCAAGT 135
Db 124 ATCTACCGGTGACAGATCTCTGCTATGACCATATCTGTAATACCTTAAACAGAGA 183
Qy 136 CTTAAGCGCTTCTCGAAGCGCTCCATGGTTCGAGCGGCTCAAGCCGAGGCAAT 195
Db 184 CTGAAACATTTGGCTTAAATTTCCAGTGTCTAGCAGGAAATGCTGTAATGAGGTCT 243
Qy 196 AGCGAGGGAACACAGGAACTTCTTTATCGTCCCTTTTGGAGACGTTCTCTGTGTGA 255
Db 244 GACGAGGTAACTGTTACCTTACAGAAATTTGTCCTGACACAAATTCAC---TTATC 300
Qy 256 GTGAAGACCTCGCGATGATCTTCAGGCGCCACGATCGAGGTATGAGAAAGCGGA 315
Db 301 GTCCAAGATCTTCGAGAGATCTGTCTGCCCAACAATGGATTTCGCTTGAAGAGCTGAC 360
Qy 316 TACCCTATGGCGATGTTTGAACGAGAACATCATCGCGCCAAAGAAAGACGTT-----ACCT 369
Db 361 TTTCTCTATCTCATGTTAGCAGAAAGACTTTTGGCCTTGTGATGACTATCAATCCACCT 420
Qy 370 ATTGACCTTGTGTTGTTCCCGACCAACCAAGCTGTAAATTTCTATTGAGCTCAACTTC 429
Db 421 GGAACACATATAGGTATGGCCCAAGAGTGGGCTGTATTTGCACTTCAAGCAAACTTT 480
Qy 430 ATCAAGGGCGGATCTATCTCTCATCTGTCACGACGACGAGCTGTATGATATGGTAGGC 489
Db 481 ATCTCGGCGGCTCTGCTTAACTATTGTGCGGACGACAAATATTATGATATAACAGGA 540
Qy 490 CAAAGTGGCTGATCGTCTACTCTCAAGGCGTGCCTAAAGCAACCTTCAACCGAAGAG 549
Db 541 CAGGAAGTATCATCACTTGTCTCAATAATCTTGGCCACCAAAACCTTTCTCTGATGA 600
Qy 550 GAAATGACCGGCCATGAACCTCGATCGCAAGACGATAGTTCTTTCCTTGAACAACTATCG 609
Db 601 GAACTCTCATTTGGAAATATAGATAAAAGCAAACTTATTTCTTTGTTGATGAACCTTGG 660

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QY 610 ATT---GGCCCCGAGGTAGATCATCATGATTTGCAAAAGCTGATGTAGCTGGTGGTGCAGCT 666
Db 661 GAAACCGGACACACCGCTAGTTTATGAAATAGTGGAAACCTCTAGAAATACAAAGTGGAGAG 720
QY 667 GTTCTCACCGCGGTCACT-----GCAAGCTGGCGGCTTCTTACATTCAGCCCCAAG 717
Db 721 GAAAAGGAACAGCTTTGTTCTCGAACTCTACTTGGGCTTATGTGAAATTTTCTGCTATC 780
QY 718 GCATGTCAGAGCTCAAGGATGCTGTACCAAGACTCTTGAAGCATCAACAAGTTTCGTG 777
Db 781 TCATTGCAGATCTAGGATTTTGGCAATGCAGACATGATCTTCTGGCACAAAATTTGTC 840
QY 778 TCGACTGAGATGCTCTTTTGGGCTTCTATGGAATTCGGCTCTCGCGTGGCTCTCGAA 837
Db 841 TCCACTGATGATATCGTCACTGCTTCTATCGAAATCAGTTTCTCGAGCCGCTTATCT 900
QY 838 AGAATCGATGGCTCTGACCTACCGAGTTCTCGCGTGTCTGTTGATGCTCGACCGCAATG 897
Db 901 CGACTTAAACCGAAGAACGAAATCAAATTTAGGCGGTCTGTGATGTTAGAAAACGGCTA 960
QY 898 GGTGTCTCGAAACAACTTACCGAGGCTTCTTCAAACATGACCTTACCACAACTCGACCATC 957
Db 961 GGACTCCCGGAAACGATATCCAGGTTATTAGTCAACATGACCTTTTAATACAGTTTCCCTG 1020
QY 958 GCGGAATCGCCAAACGAGTCACTCGCGGCAACAGCATCAAGCTTCTGTTTCAAGACTCGAC 1017
Db 1021 AAAAGCTTGGATCATAAAAGTTTGGCGGTTCTTGCAATCAGATTGCGAGGAAGCTTAGAC 1080
QY 1018 CCGCGGAGCA-----TGGCGGAGCGAACAAGAGTCTCGGAGCTCGGAGCTGACACAAAC 1071
Db 1081 CCTAAAGTCTTCGATTTGGCTTATAATACATGCGCATGCTGCTACGCTCTTGTAGCCGATGC 1140
QY 1072 CCGCAAGCTCCAAAGTATCCCTGAGCGGTGATGCGGACCCATCTACAGCGCTCATGCTG 1131
Db 1141 CCGACAAAGCTAAGTTTCTATACCTCAACCAATGATCTTATCTCGAATTTATGGTC 1200
QY 1132 AGTTCTTGGGCGCAAGTGGGACTCTGGGATTAAGCATTTTGGGCTCGGACTGGGTAAAGCCC 1191
Db 1201 AGTTCTGGGCGCAAGTCAAGCTGTATGAGTTGATTTCAATCTAGGGCTTGGGAAGCCC 1260
QY 1192 GAGACTGAGAGCGGCAATCTTTGAGCTGTGAGCTGTGAGAGCTTGTATCTTTATGCCCAAG 1251
Db 1261 AAGAGTGTACGAGCGGCGGCTTCATTTCCCTTGGAGGCTAATATATTTTATGCCCTAGA 1320
QY 1252 AAGCTGTATGGGAGTTCTGTGGCGGCTTCTCTGAGGAGTGAAGATATGACCGATG 1311
Db 1321 TCCTCAGAGGTGAATGTTGTTGCTCTTTGGCTTAGAGATAAAGATTGGGAGTGCCTG 1380
QY 1312 AAGCGGATAGAGGTGGACCAAGTATGC 1340
Db 1381 AATCGGATAAAGATGGACAAATTTATGC 1409
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RESULT 10

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US-10-614-954-7
; Sequence 7, Application US/10614954
; Publication No. US20040034884A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/614,954
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
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; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 7
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; US-10-614-954-7
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Query Match 18.4%; Score 249.8; DB 16; Length 1425;

Best Local Similarity 51.9%; Pred. No. 3.6e-75;

Matches 700; Conservative 0; Mismatches 622; Indels 27; Gaps 5;

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QY 16 CAGCTCGACACCTCGGCCAGCTACGAGGCTCCCTTTCGATCTACACCCAAATCACTCTC 75
Db 64 CAACCTTGATATTTTGGGACAAACCTTCGCTATACAAACTATACACTCAATATGCTCT 123
QY 76 CTCTACCCCGTCTCTGATTTCTCTCAATATCCACTATTGTGAGCACTTTCGAGCAAGGT 135
Db 124 ATCTACCGGTGTACAGATCTTCTGCTCATGACCATATCGTAAATACCTTTAAACAAGGA 183
QY 136 CTTAAGCGCTTCTCGAAGCGGTCCCATGGGTGCGAGCCAGGTCAAAGCGGAGGCAAT 195
Db 184 CTTGAAACATTTGGCTTAAATAATTTCCAGTGGCTAGCAGGAAATGTCGTAATGAAGGTCT 243
QY 196 AGCGAGGGAACACAGGACTTCTTATCGTCCCTTTTGGAGACGTTCTCTGTTGTA 255
Db 244 GACGAAGGTAAACACTGGTACCTACAGATTTGTCGCTCAGACAAATTCAC---TTATC 300
QY 256 GTGAAAGACTCCGCGATGATCTTTCAGCGGCCACGATCGAGGATATGAAAGCGCGGA 315
Db 301 GTTCAAGATCTTCGAGAGATCTGTCTGCCCAACATGATGGATTCGTTGAAAAGCTGAC 360
QY 316 TACCTATGGCGATGTTTGAAGAAACATCATCGCGGCCAAGGAAGACGTT-----ACCT 369
Db 361 TTTCTCTATCTACATGTTAGACGAAAAGACTTTTGGCGCTTGCATGACTATCAATCCACCT 420
QY 370 ATTGACCTGTGTGTTGTCGCCAGCACCAAGCCCTGTAATTTCTATTGAGCTCACTTC 429
Db 421 GGAACACATATAGGTATGGCCGCCAAGAGTGGCGCTGTATTTGCACTTCAAGCAAACTTT 480
QY 430 ATCAAGGGGGGACTCATCTCTCATCTGCAACGACGACGAGTGTATGATATGTTAGGC 489
Db 481 ATCTCGGGCGGCTGTCTTAACTATTGTGCGGCGAGCACAATATATGATATAACAGGA 540
QY 490 CAAGATGCGGTGATCGTCTACTCTTCAAGCGGTGCGGTAACGACCCATTCACCGAAGAG 549
Db 541 CAGGAAAGTATCATCAACTTGTCTCAATAATCTTGCACCAAAAACCTTTCTCTGATGA 600
QY 550 GAAATGACGGCCATGAACCTCGATCGAAGACGATAGTTTCTTACCTTCAAAAACATACG 609
Db 601 GAACTGCTCATTTGGAATAATAGATAAAAGCAATCTATTCTCTTGTGTTGATGAAACTTGG 660
QY 610 ATT---GGCCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGGTGCAGCT 666
Db 661 GAAACCGGACACACCGCTAGTTTATGAAATAGTGGAAACCTCTAGAAATACAAAGTGGAG 720
QY 667 GTTCTCACCGCGGTCACT-----GCAAGCTGGCGGCTTCTTCACTTCACTTACGCCCAAG 717
Db 721 GAAAAGGAACAGCTTGTGTTCTTTCGAACTCTACTTGGGCTTATGTTGAAATTTTCTGCTATC 780
QY 718 GCATGTCAGAGCTCAAGGATGCTGTACCAAGACTCTTGAAGCATCAACAAGTTTCGTG 777
Db 781 TCATTGCAGATCTGAGGATTTTGGCAATGCAGACATGATCTTCTGGCACAAAATTTGTC 840
QY 778 TCGACTGAGATGCTCTTTTGGGCTTCTATGGAATTCGGCTCTCGCGTGGCTCTCGAA 837
Db 841 TCCACTGATGATATGCTCACTGCTTCTATCGAATTCAGTTTCTCGAGCCGCTTATCT 900
QY 838 AGAATCGATGGCTCTGACCTACCGAGTTCTCGCGTGTCTGTTGATGCTCGACCGCAATG 897
Db 901 CGACTTAAACCGAAGAACGAAATCAAATTTAGGCGGTGTGTGATGTTAGAAAACGGCTA 960
QY 898 GGTGTCTCGAAACAACTTACCGAGGCTTCTTCAAACATGACCTTACCACAACTCGACCATC 957
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Db 961 GGACTCCCGAAACGATATCCAGGTTATTAGTCAACATGACCTTTAATACAGGTTCCCTG 1020
Qy 958 GCGGAAATCGCAACGAGTCACTCGCGCAACAGAGTACAGCTTCGTTTCAGAACTCGAC 1017
Db 1021 AAAAGCTTGGATCATAAAGTTTGGCGGTTTTCATACACAGATTTCGACAGGAGCTAGAC 1080
Qy 1018 CCGCGGAGCA-----TGGCCGAGCGAAACAGAGGTCTCGCAGCTTACCTGACACAAAC 1071
Db 1081 CTTAAAGTCTTCGATTGGCCCTAATATACATGCGCATTGCTACGCTCTTTAGCCGATGC 1140
Qy 1072 CCGCAAGTCAACAGTATCCCTGACGGCTGATGCGGACCCATCTACAGCCTCATGCTG 1131
Db 1141 CCGCAAGACTAAGGTTTCTATACCTCAACAAATTGATCTTATCTGGAATTATGCTG 1200
Qy 1132 AGTTCTTGGCCCAAGTGGGACTCTGGGATTACGATTGGGCTCGGACTGGGTAAGCC 1191
Db 1201 AGTTCTTGGCCCAAGTGGGACTCTGGGATTACGATTGGGCTCGGACTGGGTAAGCC 1260
Qy 1192 GAGACTGTGAGACGGGCAATCTTTGAGCCTGTTGAGAGCTTGTATGATCTTTATGCCAAG 1251
Db 1261 AAGAGTGTACGACGGCGGCTTCATTTCCCTTGAGAGCTAATATATTTATGCTAGA 1320
Qy 1252 AAGCCTGTATGGCGAGTCTGTGCGGCTTTCTCTGAGGAGTATGAGATGACCGATTG 1311
Db 1321 TCTCCAGAGGTCAAAATGGTGTGCTCTTTGCTTTAGAGATAAAGATTGGGAGTGCCTG 1380
Qy 1312 AAGCGGTAAGGAGTGGACCAAGTATGC 1340
Db 1381 AATGGGATAAAGATGGCAAAATATGC 1409

RESULT 11

US-10-653-047-4594

; Sequence 4594, Application US/10653047

; Publication No. US20040229367A1

; GENERAL INFORMATION:

; APPLICANT: Randy M. Berka

; APPLICANT: Michael W. Rey

; APPLICANT: Jeffrey R. Shuster

; APPLICANT: Sakari Kauppinen

; APPLICANT: Ib Groth Clausen

; APPLICANT: Peter Bjørke Olsen

; TITLE OF INVENTION: Methods For Monitoring Multiple Gene

; FILE REFERENCE: 5849, 200-US

; CURRENT APPLICATION NUMBER: US/10/653,047

; PRIOR FILING DATE: 2003-08-29

; PRIOR FILING DATE: 2000-03-22

; PRIOR FILING DATE: 1999-03-22

; NUMBER OF SEQ ID NOS: 7860

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4594

; LENGTH: 695

; TYPE: DNA

; ORGANISM: Aspergillus oryzae

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(695)

; OTHER INFORMATION: n = A,T,C or G

US-10-653-047-4594

Query Match 10.8%; Score 146.2; DB 18; Length 695;
Best Local Similarity 57.5%; Pred. No. 2.3e-39;
Matches 325; Conservative 0; Mismatches 225; Indels 15; Gaps 3;
Qy 5 CTTTAAAGATACAGCTCGACACCTCGGCCAGTACAGGCTCTCTTTCGATCTACACCC 64
Db 109 CATTACATGTAAGCTGAACTTCTTGGGTGAGTGTGCTGCTC---AGGATCTACACGC 165
Qy 65 AATACATCTCTCTACCCCGTCTCTGATTCCTCTCAATATCCACTATTGTGACGACCT 124

Db 166 AAATCTGCTCTGCTTTCGGTTC---GATGCTCATCTGATCAAGAGATAGTACGAGCC 222
Qy 125 TCGAGCAAGTCTTAAAGCGCTTCTCCGAAAGCGTCCCATGGTTCGAGCCAGGTCAAAG 184
Db 223 TAGAGATGGCTCGAAGAGTGTCCACCAATTTCCCGTGGTAGCAGCCAGATAGTCA 282
Qy 185 CCGAGGCAATTAGCGAGGAAACACAGGAATTCCTTTATCGTCCCTTTTGGAGGACGTT 244
Db 283 GTGAAGGCGAGCAGCCACAAACATCTGGCACATTCATGATCAAGCACTGGGGAAGACTC 342
Qy 245 CTCGTGTTGTAGTGAAGACCTCGCGATGATCTTTCAGCGCCACAGATCGAGGATGTA 304
Db 343 CACCACTGTTGTGAAGACTTCCTGTCATGATCCGAGCTTCGACCAATGACGATTTGA 402
Qy 305 GAAAGCGCGATACCTATGCGATGTTTGACGAAACATCATCGCGCCAAAGGAAGACT 364
Db 403 GACGCGCGACTTTCCTTTCCGATGTTAGAGAGAAACATCATTTGCTCCTCGGAAACCT 462
Qy 365 TACCTATTGGACCTGATGATCGTCCGACGAGCCAAAGCTGTATTTCTATTGACGTCA 424
Db 463 TGCCAA-----GCCCTGACGAAGATATTTCTCACCGGCTTTCTTGTCCAGGCTA 513
Qy 425 ACTTCATCAAGGCGGACTCATCTCACTGTCAACGAGACAGCGTGTATGATATGG 484
Db 514 ATTNTATTACGCGCGGCTGCTCCTCATCTTTGTGGCCATCATAGCAATGACATGA 573
Qy 485 TAGGCAAGATGCGGTGATCGTCTACTCTCAAGCGTTCGCGTAACGACCCATTTCACCG 544
Db 574 CTGGTCANGACAGGTTATCCACCTTCTCTCGAAGCATGTCGTGGGATACATATACA 633
Qy 545 AAGAGAAATGACGCCATGAACCT 569
Db 634 GATTGGAGTAGAGTCAGGGAACCT 658

RESULT 12

US-10-369-493-27681/C

; Sequence 27681, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; PRIOR FILING DATE: 2003-02-28

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 27681

; LENGTH: 1947

; TYPE: DNA

; ORGANISM: Neurospora crassa

US-10-369-493-27681

Query Match 2.9%; Score 39.2; DB 15; Length 1947;
Best Local Similarity 53.2%; Pred. No. 0.055;
Matches 83; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
Qy 1050 CCGCAGTACCTGCGACAAACCCGACAAAGTCCAAAGTATCCCTGACCGCTGATCGGA 1109
Db 1854 CCGCAGTACCTGCGACACACCGATGATGACAAAGTGTAAATGCGCGCTGTGGCG 1795
Qy 1110 CCATCTACAGCTCATCTGAGTCTTGGGCGAGTGGGACTCTGGGATTCGACTT 1169
Db 1794 CGCTGGAACCTGCGCTTCTGATGTTGATGCGAACGTCGCGCTCTTCCGCTCCGACTC 1735
Qy 1170 TGGGCTCGGACTGGGTAAAGCCGAGACTGTGAGACG 1205

Db 1734 GTAAATGGGCTGTCAAGCTGACAAAGGTGAAGG 1699

RESULT 13

US-10-767-701-11710
; Sequence 11710, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 11710
; LENGTH: 688
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(688)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS13347_1
US-10-767-701-11710

Query Match 2.7%; Score 36.4; DB 17; Length 688;

Best Local Similarity 47.4%; Pred. No. 0.31;
Matches 109; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 940 TACCACAACTCGACCATCGGCGAAATCGCCACAGTCACTCGGCGCAACAGCATCACGC 999
DB 20 TAAGTCACTACCCCTTGAGGTCCGGTCAGGCTGCTCAAGCTCAATTGTACTGTGT 79
QY 1000 CTTGCTTCAGAACTCGACCCCGGAGCATGCGCCAGCGAAAGAGGTCTCGGAGGTAC 1059
DB 80 CAGCGGAAGAAAGAGAGACACTCCAGCTCCGGGGCTCCAGAGATCGAGCGCAAG 139
QY 1060 CTGCACAAACCCGACAGTCAAGTATCCCTGACGGCTGATCGGACCCATCTACC 1119
DB 140 ATGAAGAGGGCAACGCGAATCGTCGACATCTCATGCCATCATCTCCCTCTC 199
QY 1120 AGCGTCATGCTGAGTTCTTGGGCAAGGTGGGACTCTGGGATTACGACTT 1169
DB 200 GGGCTTCTCAAGTTCGGCTCAAGGTGAGTTCTGGCTCTGCTCTT 249

RESULT 14

US-10-767-701-11709
; Sequence 11709, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 11709
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS13347_2
US-10-767-701-11709

Query Match 2.7%; Score 36.2; DB 17; Length 684;

Best Local Similarity 47.6%; Pred. No. 0.36;
Matches 107; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 945 CAACTCGACCATCGGCGAAATCGCCAAACGAGTCACTCGGCGCAACAGCATCAGCCCTTCG 1004
DB 17 CCATACACCCCTTGGAGCTCCCGGTCAAGCTCAATTGTACTGTGTGTCAGCG 76
QY 1005 TTCAGAACTCGACCCCGGAGCATGCGCCAGCGAAACAAGGCTCTCGGACGACTCTGCA 1064
DB 77 GGAAGAAAGAGAGACACCTCCAGCTCCGGGGCTCCAGAGATCGAGCGCAAGTAA 136
QY 1065 CAACACCCCGACAGTCCAACTATCCCTGACGGTGTATGCGGACCCATCTACCGCT 1124
DB 137 GGAGGCGACGGCGAATCTGCTGACATCTCATCGCATCATCTCCCTCTCTCGGCGT 196
QY 1125 CATGCTGAGTTCTTGGGCCAAAGTGGGACTCTGGGATTACGACTT 1169
DB 197 CTTCTCAAGTTCGGCTGCAAGGTGAGTTCTGGCTCTGCTCTT 241

RESULT 15

US-10-425-115-66302
; Sequence 66302, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 66302
; LENGTH: 1707
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_160468C.1
US-10-425-115-66302

Query Match 2.7%; Score 36; DB 18; Length 1707;

Best Local Similarity 48.1%; Pred. No. 0.67;
Matches 102; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 14 TACAGCTCGACACCCCTCGGCGAGCTACAGGCTCTTTTCGATCTACACCCCAATCAGTC 73
DB 307 TCCGCGCTCCCTCCCGCTCCACCTCCACTCGCTCCACCCACCCCTCCCTC 366
QY 74 TCCTCTACCCCGTCTCTGATTCTCTCAATATCCCACTATTGTTCAGCACCTTCGAGCAAG 133
DB 367 CCTTACCGCTCGCTCTTTCGGGAGCGGAGGAGATCACCAGGAGGGGGGAGGACG 426
QY 134 GTCTTAAGCGCTTCTCCGAAGCGGTCCCATGGTTCGAGGCCAGGTCAAAGCCGAGGCA 193
DB 427 ACCTTCTCCCTCGGCGGGGGCGGAGGGGAGGAGGCGAGGCGATGGTGGGGCG 486
QY 194 TTAGCGGGAACACACAGGAATCTCTTATC 225
DB 487 AGGGCGACGCGAGCGAGGGCGACTCGGTCAAC 518

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Job time : 825 secs

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OM nucleic - nucleic search, using sw model

Run on: January 23, 2005, 13:23:58 ; Search time 138 Seconds
(without alignments)
6984.273 Million cell updates/sec

Title: US-10-614-954-5
Perfect score: 1356
Sequence: 1 atgggtttcaagatacagct.....atgcgacgtacgttggttag 1356

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1356	100.0	1356	3	US-09-538-414-5
2	1356	100.0	1356	4	US-10-074-279-5
3	915.6	67.5	1403	3	US-09-538-414-1
4	915.6	67.5	12949	3	US-10-074-279-1
5	915.6	67.5	12949	3	US-09-538-414-11
6	915.6	67.5	12949	4	US-10-074-279-11
7	915.6	67.5	13737	3	US-09-538-414-10
8	915.6	67.5	13737	4	US-10-074-279-10
9	249.8	18.4	1425	3	US-09-538-414-7
10	249.8	18.4	1425	4	US-10-074-279-7
11	39.8	2.9	4403765	3	US-09-103-840A-2
12	39.8	2.9	4411529	3	US-09-103-840A-1
13	36.6	2.7	834	4	US-09-621-976-2574
14	34.2	2.5	720	4	US-09-252-991A-16032
15	34.2	2.5	1074	4	US-09-252-991A-16568
16	34.2	2.5	2721	4	US-09-252-991A-16144
17	34	2.5	1713	4	US-09-540-236-1014
18	34	2.5	269223	4	US-09-596-002-41
19	33.4	2.5	516	4	US-09-252-991A-15293
20	33.4	2.5	1614	4	US-09-252-991A-15438
21	33.2	2.4	399	4	US-09-621-976-8976
22	33	2.4	832	4	US-09-621-976-2813
23	32.8	2.4	1230025	4	US-09-198-452A-1
24	32.4	2.4	1620	3	US-09-125-642C-9
25	32.4	2.4	1740	3	US-09-125-642C-2
26	32.4	2.4	1742	3	US-09-125-642C-13
27	32.4	2.4	5515	3	US-09-125-642C-8

ALIGNMENTS

RESULT 1
US-09-538-414-5
; Sequence 5, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Fusarium graminearum
US-09-538-414-5

Query Match	100.0%;	Score 1356;	DB 3;	Length 1356;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1356;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGGGCTTTCAAGATACAGCTCGACACCCCTCGGCGAGCTACACAGGCTCTCTTCGATCTAC	60	
Db	1	ATGGGCTTTCAAGATACAGCTCGACACCCCTCGGCGAGCTACACAGGCTCTCTTCGATCTAC	60	
QY	61	ACCCAATCAGTCTCTCTTACCCGCTCTGATCTCTCAATATCCCACTATTGTGAGC	120	
Db	61	ACCCAATCAGTCTCTCTTACCCGCTCTGATCTCTCAATATCCCACTATTGTGAGC	120	
QY	121	ACCTTCGACACAGGCTTTAAGCGCTTCTCGAAGCCGTCCTCGGTCGCGCCGAGGTC	180	
Db	121	ACCTTCGACACAGGCTTTAAGCGCTTCTCGAAGCCGTCCTCGGTCGCGCCGAGGTC	180	
QY	181	AAAGCCGAGGCGATTAGCGAGGAAACACAGAACTTCTCTTATCGTCCCTTTTGAGGAC	240	
Db	181	AAAGCCGAGGCGATTAGCGAGGAAACACAGAACTTCTCTTATCGTCCCTTTTGAGGAC	240	
QY	241	GTTCTCGTGTGTAGTGAAGACCTTCCGCGATGATCTTTCAGCGCCACGATCGAGGCT	300	
Db	241	GTTCTCGTGTGTAGTGAAGACCTTCCGCGATGATCTTTCAGCGCCACGATCGAGGCT	300	
QY	301	ATGAGAAAGCGCGGATACCTTATGGCGATGTTTGAGGAAACATCATCGGCCCAAGAG	360	
Db	301	ATGAGAAAGCGCGGATACCTTATGGCGATGTTTGAGGAAACATCATCGGCCCAAGAG	360	

Db 301 ATGAGAAAGCGGGATACCTATGGCGATGTTTGACGAGAAATCATCATCGGCCCAAGGAG 360
Qy 361 AGCTTACCTATTGGACCTGCTACTGCTCCGACGACCCAAAGCCTGTAATCTATTGACG 420
Db 361 AGCTTACCTATTGGACCTGCTACTGCTCCGACGACCCAAAGCCTGTAATCTATTGACG 420
Qy 421 CTCAACTTCATCAAGGGCGAGCTCATCTCTCACTGTCAACGGACAGCACGGTCTATGGAT 480
Db 421 CTCAACTTCATCAAGGGCGAGCTCATCTCTCACTGTCAACGGACAGCACGGTCTATGGAT 480
Qy 481 ATGGTAGGCAAGATCGGTGATCCGTCTACTCTCAAGCGGTGCGTAACACCCATTTC 540
Db 481 ATGGTAGGCAAGATCGGTGATCCGTCTACTCTCAAGCGGTGCGTAACACCCATTTC 540
Qy 541 ACCGAGAGGAATGACGGCCATGACCTCGATCGCAAGCAGATGTTCTTACCTTGA 600
Db 541 ACCGAGAGGAATGACGGCCATGACCTCGATCGCAAGCAGATGTTCTTACCTTGA 600
Qy 601 AACTATACGATTGGCCCGAGGTAGATCATCAGATTGTCAAAGCTGANTAGTGTGT 660
Db 601 AACTATACGATTGGCCCGAGGTAGATCATCAGATTGTCAAAGCTGANTAGTGTGT 660
Qy 661 GAGCTGTCTTCAAGCGGTGATGCAAGTGGGGTCTTTCATATTGACCCCAAGGC 720
Db 661 GAGCTGTCTTCAAGCGGTGATGCAAGTGGGGTCTTTCATATTGACCCCAAGGC 720
Qy 721 ATGTACAGCTCAAGATGCTGTACCAAGACTCTTGAAGCTCAACAAAGTTCTGTGTCG 780
Db 721 ATGTACAGCTCAAGATGCTGTACCAAGACTCTTGAAGCTCAACAAAGTTCTGTGTCG 780
Qy 781 ACTGACGATGCTCTTTTCGGGTTTCACTGGAATCGGCCCTCTCGGTGGTCTCGAAGA 840
Db 781 ACTGACGATGCTCTTTTCGGGTTTCACTGGAATCGGCCCTCTCGGTGGTCTCGAAGA 840
Qy 841 ATCGATGGCTTGCACCTACCGAGTCTGCGGTGCTGTTGATGCTCGACGGCAATGGT 900
Db 841 ATCGATGGCTTGCACCTACCGAGTCTGCGGTGCTGTTGATGCTCGACGGCAATGGT 900
Qy 901 GTCTCGAAACACTPACCCAGGCTCTTCAAACATGACCTACCAACATCGACCTCGACCTCGC 960
Db 901 GTCTCGAAACACTPACCCAGGCTCTTCAAACATGACCTACCAACATCGACCTCGC 960
Qy 961 GAAATCGCCAAAGAGTCACTCGCGGCAACAGCATACGCGCTTGGTTCAGAACTCGACCC 1020
Db 961 GAAATCGCCAAAGAGTCACTCGCGGCAACAGCATACGCGCTTGGTTCAGAACTCGACCC 1020
Qy 1021 GCGAGATGCGCCAGGCAACAGAGTCTCGGACGTCTCGACAAACACCCCGACAG 1080
Db 1021 GCGAGATGCGCCAGGCAACAGAGTCTCGGACGTCTCGACAAACACCCCGACAG 1080
Qy 1081 TCCAAAGTATCCCTGACGGCTGATCGGACCCATCTACAGCGTCACTGAGTTCCTGG 1140
Db 1081 TCCAAAGTATCCCTGACGGCTGATCGGACCCATCTACAGCGTCACTGAGTTCCTGG 1140
Qy 1141 GCGAAGTGGGACTCTGGGATACGATTTGGGCTCGAGTGGGTAAAGCCGAGACTGTG 1200
Db 1141 GCGAAGTGGGACTCTGGGATACGATTTGGGCTCGAGTGGGTAAAGCCGAGACTGTG 1200
Qy 1201 AGACGGCCATCTTTGAGCTGTGAGAGCTTGAATGATCTTTATGCCAAGAGCCTGAT 1260
Db 1201 AGACGGCCATCTTTGAGCTGTGAGAGCTTGAATGATCTTTATGCCAAGAGCCTGAT 1260
Qy 1261 GCGAGTCTGTGCGGCGCTTCTCTGAGGGATGAGGATATGACCGATTGAGGGCGGAT 1320
Db 1261 GCGAGTCTGTGCGGCGCTTCTCTGAGGGATGAGGATATGACCGATTGAGGGCGGAT 1320
Qy 1321 AAGGAGTGGACCAAGTATGCGAGTACGTTGGTTAG 1356
Db 1321 AAGGAGTGGACCAAGTATGCGAGTACGTTGGTTAG 1356

RESULT 2
US-10-074-279-5

; Sequence 5, Application US/10074279
; Patent No. 6646184
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Fusarium graminearum
US-10-074-279-5

Query Match 100.0%; Score 1356; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTTTTCAGATACAGCTCGACACCTCGGCCAGCTACAGGGCTCTCTTTTCGATCTAC 60
Db 1 ATGGCTTTTCAGATACAGCTCGACACCTCGGCCAGCTACAGGGCTCTCTTTTCGATCTAC 60
Qy 61 ACCCAATACAGTCTCTTACCCCGTCTCTGATTCCTCTCAATATCCCAATTTGTCAGC 120
Db 61 ACCCAATACAGTCTCTTACCCCGTCTCTGATTCCTCTCAATATCCCAATTTGTCAGC 120
Qy 121 ACCTTCGAGCAAGTCTTAAAGCGCTCTCCGAGCGGTCCCATGGTTCGACGGCCAGGTC 180
Db 121 ACCTTCGAGCAAGTCTTAAAGCGCTCTCCGAGCGGTCCCATGGTTCGACGGCCAGGTC 180
Qy 181 AAAGCCGAGGGCATTTAGCGAGGAAACACAGAACTTCTTTATCGTCCCTTTTCAGGAC 240
Db 181 AAAGCCGAGGGCATTTAGCGAGGAAACACAGAACTTCTTTATCGTCCCTTTTCAGGAC 240
Qy 241 GTTCTCTGTTGTAGTGAAGACCTCCGCGATGATCTTCAAGCGCCACGATCGAGGT 300
Db 241 GTTCTCTGTTGTAGTGAAGACCTCCGCGATGATCTTCAAGCGCCACGATCGAGGT 300
Qy 301 ATGAGAAAGCGGGATACCTATGCGATGTTTGACGAGAACATCATCGGCCAAGGAG 360
Db 301 ATGAGAAAGCGGGATACCTATGCGATGTTTGACGAGAACATCATCGGCCAAGGAG 360
Qy 361 AGTTTACCTATTGGACCTGTTACTGCTCCGACGACCCAAAGCCTGTAATCTATTGACG 420
Db 361 AGTTTACCTATTGGACCTGTTACTGCTCCGACGACCCAAAGCCTGTAATCTATTGACG 420
Qy 421 CTCAACTTCATCAAGGGCGAGCTCATCTCTCACTGTCAACGGACAGCACGGTCTATGGAT 480
Db 421 CTCAACTTCATCAAGGGCGAGCTCATCTCTCACTGTCAACGGACAGCACGGTCTATGGAT 480
Qy 481 ATGGTAGGCAAGATCGGTGATCCGTCTACTCTCAAGCGGTGCGTAACACCCATTTC 540
Db 481 ATGGTAGGCAAGATCGGTGATCCGTCTACTCTCAAGCGGTGCGTAACACCCATTTC 540
Qy 541 ACCGAGAGGAATGACGGCCATGACCTCGATCGCAAGCAGATGTTCTTACCTTGA 600
Db 541 ACCGAGAGGAATGACGGCCATGACCTCGATCGCAAGCAGATGTTCTTACCTTGA 600
Qy 601 AACTATACGATTGGCCCGAGGTAGATCATCAGATTGTCAAAGCTGANTAGTGTGT 660
Db 601 AACTATACGATTGGCCCGAGGTAGATCATCAGATTGTCAAAGCTGANTAGTGTGT 660
Qy 661 GAGCTGTCTTCAAGCGGTGATGCAAGTGGGGTCTTTCATATTGACCCCAAGGC 720

Db 661 GAGCGTGTCTCAAGCGGTGAGTGAAGCTGGCGGTCTTTCACATTCAGCCCCAAGGCC 720
Qy 721 ATGTCAAGATCAAGGATGCTGTACCAAGATCTTTAGCGATCAACAAGTTGCTGCG 780
Db 721 ATGTCAAGATCAAGGATGCTGTACCAAGATCTTTAGCGATCAACAAGTTGCTGCG 780
Qy 781 ACTGACATGCTCTTTTCGGCGTTCACTGGAATCGGCTCTCGCGTCTCGAAGA 840
Db 781 ACTGACATGCTCTTTTCGGCGTTCACTGGAATCGGCTCTCGCGTCTCGAAGA 840
Qy 841 ATCGATGGCTCTGCACCTACCGAGTTCTGCGGTCTGTTGATGCTCGACCGCAATGGGT 900
Db 841 ATCGATGGCTCTGCACCTACCGAGTTCTGCGGTCTGTTGATGCTCGACCGCAATGGGT 900
Qy 901 GTCTCGAACAACCTACCGAGCTTCTTCAAAACATGACCTACCAAACTCGACCATCGGC 960
Db 901 GTCTCGAACAACCTACCGAGCTTCTTCAAAACATGACCTACCAAACTCGACCATCGGC 960
Qy 961 GAAATCGCAACGAGTCACTCGCGCAACAGCATCAAGCTTCTGTTCAAACTCGACCCC 1020
Db 961 GAAATCGCAACGAGTCACTCGCGCAACAGCATCAAGCTTCTGTTCAAACTCGACCCC 1020
Qy 1021 GCGAGATCGCGCAGCAAGAGTCTCGCGAGTCTGCGAGTCTGACAAACCCGCAAG 1080
Db 1021 GCGAGATCGCGCAGCAAGAGTCTCGCGAGTCTGCGAGTCTGACAAACCCGCAAG 1080
Qy 1081 TCCAAAGTATCCCTGACGCTGATGCGGACCCATCTACAGGCTCATGCTGAGTTCTTGG 1140
Db 1081 TCCAAAGTATCCCTGACGCTGATGCGGACCCATCTACAGGCTCATGCTGAGTTCTTGG 1140
Qy 1141 GCCAAGTGGGACTCTGGGATACGACTTTGGGCTCGGACTGGGTAAGCCGAGACTGTG 1200
Db 1141 GCCAAGTGGGACTCTGGGATACGACTTTGGGCTCGGACTGGGTAAGCCGAGACTGTG 1200
Qy 1201 AGACGGCCATCTTTGAGCTGTTGAGCTGATGATCTTTATGCCCCAAGAGCTGAT 1260
Db 1201 AGACGGCCATCTTTGAGCTGTTGAGCTGATGATCTTTATGCCCCAAGAGCTGAT 1260
Qy 1261 GCGAGTCTGCTGCGGCTTCTCTGAGGATGAGGATGAGCGATGAGCGGAT 1320
Db 1261 GCGAGTCTGCTGCGGCTTCTCTGAGGATGAGGATGAGCGATGAGCGGAT 1320
Qy 1321 AAGGAGTGACCAAGTATGCGAGTACGTTGGTTAG 1356
Db 1321 AAGGAGTGACCAAGTATGCGAGTACGTTGGTTAG 1356

RESULT 3
US-09-538-414-1
; Sequence 1, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/09/538,414
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Fusarium sporotrichioides
US-09-538-414-1

Query Match 67.5%; Score 915.6; DB 3; Length 1403;

Best Local Similarity 80.3%; Pred. No. 1.1e-283;
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;
Qy 3 GCGTTTCAAGATACAGCTCGACACCTCGGCGAGCTTACAGGCTCTCTTTTGCATCTACAC 62
Db 36 GTCCTTTGATAGATGAGTCAATCATCGGCGAGCAACCGCTCTCTTTTCAATCTACAC 95
Qy 63 CCAAATCAAGTCTCTTACCCCGTCTCTGATTTCTCTCAATATCCACATTTATGTTCAGCAC 122
Db 96 CCAGATCACTCTGTTTACCCCGTCTCTGATCCCTCCAGATTCACACCATGTCAGCAC 155
Qy 123 CTTGAGCAGAGTCTTTAGCGCTTCTCGAAAGCGCTCCCATGGTTCGACGAGCCAGGTCAA 182
Db 156 CTTGAGGAGAGCCCTAAACCGCTCTCTCAAAACCTTCCCATGGTTCGCGGCGAGGTCAA 215
Qy 183 AGCCGAGGCGATTAGCGAGGGAACACAGAGAACTTCTCTTTATTCGTCCTTTTGGAGACGT 242
Db 216 GACCGAGGCGCATCGGAGAGGAACACAGAGAACTTCCAGATCATTTCCATATGAGGAGAC 275
Qy 243 TCCTCGTGTGTAGTGAAGACCTCGCGATGATCTTTCAGGCGCCACGATCGAGGGTAT 302
Db 276 ACCCGCTCTTGTGGTGAAGACCTCCGTGATGATTCCTCAGGCGCCAAACGATCGAGGGT 335
Qy 303 GAGAAAGCGGATACCTTATGCGGATGTTTTCAGGAGACATCATCGCGCCAGGAAGAC 362
Db 336 GAGAAAGCGGGTTCCTCCCTTAGAGATGTTTTCAGAGAACTGCTCGCTCCGAGGAGAC 395
Qy 363 GTTACCTATTGACCTTGGTACTTGGTCCCGACGACCCAAAGCTGTAAATTTCTATTGACGCT 422
Db 396 ATTAGTATCGACCTTGGCAATGGCCCCAAGCGGAGCTGTGTGCTATTGCGCT 455
Qy 423 CAACTTCATCAAGGCGGACTCATCTCACTGTCAACGAGACGACGCTGTGTATGATAT 482
Db 456 CAACTTCATCAAGGCGGACTCATCTCACTGTCAACGAGACGACGCTGTGTATGATAT 515
Qy 483 GGTAGCCAGATGCGGTGATCGGTCTACTCTTCCAGGCGTCCGCTTAAAGCCCATTCAC 542
Db 516 GACAGGACAAAGATGCAATTTATTTCTCTTCCAAAGGCGTCCGCAACGAAATCATTCAC 575
Qy 543 CGAAGAGGAAATGACGGCCATGAACTCGATCGCAAGACGATAGTTCTTACCTTCAAAA 602
Db 576 CGAGGAGGAAATCTCGGCCATGAACTCGATCGCAAGACGCTAGTCCCTCTCTTGA 635
Qy 603 CTATAGATTTGCCCGGAGGTAGATCATCAGATTTCAAAGCTGTATGCTGTGCTGTA 662
Db 636 CTACAAAGTTGGTCTCTGAGCTAGACACAGATCGCAAAACCTTTCGCTGCTGCGCA 692
Qy 663 CGCTGTTCTCAGCGGCTCAGTGAAGCTGGGCTTCTTCAATTCAGCGCCCAAGGCCAT 722
Db 693 CGCTCCACCGGACCGGCCAAGGCAAGCTGGGCTTCTTTCATTCATTCCTCCCAAGGCCCT 752
Qy 723 GTGAGAGCTCAAGGATGCTGTACCAAGACTCTTGACGATCAACAAAGTTCTGTGTGAC 782
Db 753 CTGCGAGCTGAAGACGACGACCAAGACTCTTGACGCTGTCCAAAGTTGTGTCAAC 812
Qy 783 TGACGATGCTCTTTTGGGCTTCACTGGAATTCGGCTCTCGCGTGTGCTGAAAGAT 842
Db 813 TGATGATGCTCTTTGGGCTTCACTGGAATTCGGCTCTCGCGTGTGCTGCAAGAT 872
Qy 843 CGATGGCTCTGACCTACCGAGTTCTGCGCTGTGTGATGCTCGACCGGCAATGGGTGT 902
Db 873 GGATGCTTCCACACCTACTGAAATTCGCGCGCTGTGCAATGCGGGGCGCCCAATGGGCGT 932
Qy 903 CTCGAACACTTACCAGGCTTCTTCAAAACATGACCTACCAAACTCGACCATCGGCGA 962
Db 933 ATCAAGCATATACCGGCTTCTTCAAAACATGACCTACCAATGACTCGACCGTCCCGCA 992
Qy 963 AATCGCCAAAGGATCACTCGGCGCAACAGCATCAAGCTTGTGCTGAGAACTCGACCCCGC 1022
Db 993 AATCGCCAAAGGATCACTTGGCGCAACAGCATCAAGCTTGTGCTGAGAACTCGACAGTGA 1052
Qy 1023 GAGCATGCGCAGCGAAGAGGTTCTCGGAGGTCTCGGAGGTACCTTGCAACAAACCCGACAGTC 1082

Db	1053	TCGTTTTGCCGACGACGAACAACAAAGCTTTGGCGAGCTATCATGCTATGGCTGCTGCTGACAAGTC	1112
Qy	1083	CAACGTTATCCCTTCAGCGCTGTACGCGACCCCAATCTACCAGCTCATCTGAGTCTCTTGGGC	1142
Db	1113	GAGCGTCTCCTTACCGCGGATCGGAATCCGTCACGACGATCATGCTGAGTCTCTGGGC	1172
Qy	1143	CAAGGTGGGACTCTGGATTPACACTTTGGCTCGGACTGGGTAAAGCCGAGACTGTGAG	1202
Db	1173	CAAGGTGGGATGCTGGGAGTATCACTTTGGGTTTGGACTGGGTAAAGCCTGAGAGTGTGAG	1232
Qy	1203	ACGGCCNAATCTTTGAGCTCTGTGAGAGCTTGATGTACTTTATGCCCAAGAAGCCTGATGG	1262
Db	1233	AAGACTCGTTTGAACCTTTTCGAGATTGTGATCTTTATGCCCAAGAAGCCTGATGG	1292
Qy	1263	CGAGTCTGTGCGGCGCTTTCTCTGAGGATGAGGATATGGACCGATTGAAGCGCGATAA	1322
Db	1293	GGAGTTTACGCGCGTCCACTTTTCTCTGAGGGATGAGGATATGGAGAGACTAAAGCGCGATGA	1352
Qy	1323	GGAGTGACCAAGTATGCGCAGTACGTTGGTTAG	1356
Db	1353	GGAGTGCACAAGTACGCAAAAGTATATTGGGTAG	1386

RESULT 4

RESULTS
US-10-074-279-1
: Sequence 1. Application US/10074279

```

; Sequence 1, Application US/100/4279
; Patent No. 6646184
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Fusarium sporotrichioides
; US-10-074-279-1

```

	Query Match	67.5%	Score 915.6	DB 4	Length 1403
	Best Local Similarity	80.3%	Pred. No. 1.1e-283		
	Matches 1087	Conservative	0	Indels 3	Gaps 17
QY	3	GGCTTTCAAGATACAGCTCGACACCGCTCGGCAGCTACGAGCGCTCCTTTGCGATCTACAC	62		
DB	36	GTCCTTTGACATAGAGCTCGACATCATCGGCAGCAACGGCCTCTCTTTTCAATCTACAC	95		
QY	63	CCAAATCATGCTCTCTATACCGCGTCTCTGATTCCTCTCAATATCCCATCTATGTTCAGCAC	122		
DB	96	CCAGATCATGCTCGTCTTATCCCGCGTCTCTGATCCCTTCCAGTGATCCCAATCATGTCAGCAC	155		
QY	123	CTTTCGAGCAAGGCTCTTAAGCGCTTCTCGGAAGCGCTCCCATGCGTGGCGAGGCCAGGTCAA	182		
DB	156	CTTTCGAGGAAGCCCTAAAGCGCTCTCTCAAACTTCCCATGGTTCGGCGGCGAGGTCAA	215		
QY	193	AGCCGAGGCGATTAGCGAGGGGAAACACAGGAACCTTCTTTATCGTCCCTTTTGGAGCAGT	242		
DB	216	GAACCGAGGCGATCAGCGAGGAGAAACACAGGAACCTTCCAGATCATTCATATGAGGAGAC	275		
QY	243	TCCTCGTGTGTAGTGAAGAAGCCTCGGCGATGATCCTTCAGGCCGCCACGATCGAGGTTAT	302		
DB	276	ACCCCGCTCTTGTGGTGAAGACCTCCGTGATGATTCCTCAGCGCCAAACGATGAGGGGTT	335		

Qy	303	GAGAAAGCGGGATACCTTAATGCGGATGTTTGA	CGAGAACATCATCGCGCCAAAGGAAGAC	362
Db	336	GAGAAAGCGGGTTTCCCCTTAGAGATGTTTGA	CGAGAACGTCGTCGTCGGAAGAAC	395
Qy	363	GTTTACCTATTGGACCTGCTGCTGCTGCTGCTG	CCGACGACCAAGCCTGTAATCTTATTGCACT	422
Db	396	ATTAGCTATCGGACCTTGGGCAATGGCCCAAC	CGACCCGGAAGCCTGTGTGCTATTGCACT	455
Qy	423	CAACTTCATCAAGGGCGGACTCATCTCTCACTGT	CTAACCGGACGACGCTGTCTATTGGATAT	482
Db	456	CAACTTCATTAAGGCGGACTCATCTCACCGTCA	ACGCAAAATGCTGTGCTATTGGACAT	515
Qy	483	GGTAGGCCAAGATGCGGTGATCGCTCTACTCTC	CAAGGCGTCCGTAAGCAACCATTCAC	542
Db	516	GACAGGACAGATGCAATTAATTCGCTCTCTC	CAAGGCGTCCGCAACGATCATTCAC	575
Qy	543	CGAAGAGGAAATCAAGCCCATGAACCTCGATCG	CAAGACGATGTTCTTACCTTGAATAA	602
Db	576	CGAGGAGGAATCTCGGCCATGAACTCGATCG	CAAGACGCTGTGCTTGAATAA	635
Qy	603	CTATACGATTTGGCCCCGAGGTAGATCATCAGAT	TTGTCAAAGCTGATGCTGTGGTGA	662
Db	636	CTACAAAGTTGCTCTGAGCTAGACCAACAGAT	CGCCAAAC---TGCGCTCTGTGGCGA	692
Qy	663	CGCTGTCTCAACCGCGTCAAGTGGCGTCTTCT	TCATATCAGCCCCCAAGGCCAT	722
Db	693	CGCTCCACCCGACCGGCCAAGCAAGCTGGGGT	CTTTTCATTCACCTCCCAAGGCCCT	752
Qy	723	GTCAAGCTCAAGGATGCTGCTACCAAGACTCT	TTGACGATCAACAAAGTTGCTGTGAC	782
Db	753	CTCGGAGCTGAAAGACGACGACCAAAAGACT	CTTTGACGCGTCTCCAAGTTGTGTCAAC	812
Qy	783	TGACGATGCTTTTGGCGTTTCATCTGGAATCG	CGCTCTCGCTGCGTCTCGAAAGAT	842
Db	813	TGATGATGCTCTTTGGCGTTTATCTGGCAAT	CAACCTCGCGGTACGCTCGCAAGAT	872
Qy	843	CGATGGCTCTGCACCTACCGAGTCTTCCGCT	GTGTTGATGTGCAACCGGCAATGGGTG	902
Db	873	GGATGCTTCCACACCTACTGAAATTCCTGCG	CGCTGTGCAATCGCGGGCCCAATGGCGT	932
Qy	903	CTCGAAACAATCCAGGCCCTTCTTCAAACAT	GATCCTACCACTCGGCGCATCGGCGA	962
Db	933	ATCAAGCACATACCCAGGCCCTTCTTCAAACA	TGACTTACCATGATCGACCGTGCCTGA	992
Qy	963	AATCGCAACGAGTCACTCGCGGCAACAGCAT	CACGCTTCTGTTCAAGACTCGACCCCGC	1022
Db	993	AATCGCCAAAGAACCACTTGGCGNACAGCAT	CACGCTGCGCTCGGAACTCAAAGTGA	1052
Qy	1023	GAGCATGCGCAGCGAAACAAGGCTTCGCGA	CGTACCTGCGACAAACCCGACAACTC	1082
Db	1053	TCGTTTGGCAGACGAACAAGCTTTGGCGAG	CTATGTCATGGCTCGCTGACAACTG	1112
Qy	1083	CAACGTATCCTGACGCTGATGCGGACCATCT	TACCAGCGTCATGCTGAGTCTTTGGGC	1142
Db	1113	GAGCGTCTCCTGACCGCGGATGCGAATCGT	CAAGCAGATCATGCTGATGTTCTTGGGC	1172
Qy	1143	CAAGTGGGACTCTGGGATTAACGCTTTGGCT	CGGACTGGGTAAGCCGAGACTGTGAG	1202
Db	1173	CAAGTGGGATGCTGGGATGATGACTTTGGCT	TTGGACTGGTAAGCCTGAGAGTGTGAG	1232
Qy	1203	ACGGCCAACTTTGAGCCTGTTGAGAGCTTGA	TGATCTTTATGCCAAAGAGCCTCATGG	1262
Db	1233	AAGACCTCGCTTTGAACCTTTGAGAGTTTGA	TGTACTTTATGCCCAAGAGCCTGTGAG	1292
Qy	1263	CGAGTCTGTGCGCGCTTTCTCTGAGGAGAT	GAGGATATGGAACCGATGAGCGGATAA	1322
Db	1293	GGAGTTTACGGCGTCCATTTCTCTGAGGAT	TAGGATATGAGAGACTAAAGCGGATGA	1352
Qy	1323	GGAGTGGAACCAAGTATGCGGATGCTGTTG	TTAG	1356
Db	1353	GGAGTGGAACCAAGTACGCAAGTATATTTGG	GATG	1386

RESULT 5

US-09-538-414-11
; Sequence 11, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 12949
; TYPE: DNA
; ORGANISM: Plasmid
US-09-538-414-11

Query Match 67.5%; Score 915.6; DB 3; Length 12949;

Best Local Similarity 80.3%; Pred. No. 4e-283;

Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

QY	3	GGCTTTCAGATACAGCTCGACACCTCGGCGAGCTACGAGGCTCTCTTTCGATCTACAC	62
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QY	63	CCAAATCAGTCTCTACCCGCTCTCTGATCTCTCAATATCCCACTATTGTTCAGCAC	122
DB	11341	CCAGATCAGTCTGTTTACCCGCTCTCTGATCTCTCCAGTATCCCACTATGTCAGCAC	11400
QY	123	CTTCGAGCAAGGTCTTAAGGGTTCTCCGAGCGCTCCATGGTCGCGAGGCGAGTCAA	182
DB	11401	CCTTGAGGAGGCTTAAACCGCTCTCTCAAACTTCCATGGTCGCGGCGAGTCAA	11460
QY	183	AGCCGAGGCAATTAGCGAGGGAACACAGGAATCTCTTATGTCCTCTTTTGGAGCGT	242
DB	11461	GACCGAGGCGATCAGCGAAGGAACACAGGAATCTTCAAGATCATTTCCATATGAGGAG	11520
QY	243	TCCTCGTGTGTAGTGAAGACCTCCGCGATGATCTTCCAGCGCCCAAGATCGAGGAT	302
DB	11521	ACCCGCTTGTGTGAAGACCTCCGCGATGATCTTCCAGCGCCCAAGATCGAGGAT	11580
QY	303	GAGAAAGCGGATACCTATGGCGATGTTTGACGAGAACATCATCGCGCCAGGAAGAC	362
DB	11581	GAGAAAGCGGATTTCCCTTAGAGATGTTTGACGAGAACCTCGCTCCGAGGAAGAC	11640
QY	363	GTTACCTATTGACCTGGTACTGGTCCGAGGACCAAGCGCTGTAATTTCTATTGCGCT	422
DB	11641	ATTAGCTATCGGACCTTGGCAATGGCCCAAGCGGAGCGCTGTTGCTATTGCGCT	11700
QY	423	CAACTTTCATAGGGCGGACTCATCTCTCATCTGTCAACGGACAGCGTCTGATGATAT	482
DB	11701	CAACTTTCATAGGGCGGACTCATCTCTCACCGTCAACGGACAGCGTCTGATGATAT	11760
QY	483	GGTAGCCCAAGATGCGGTGATCGTCTATCTTCAAGGGGTCGCGTAACGCCATTAC	542
DB	11761	GACAGGACCAAGATGCAATATTGCTCTCTCTCAAGGGGTCGCGTAACGCCATTAC	11820
QY	543	CGNAGGAGAAATCAGCGCCATGAACCTCGATCGCAGAGCGATGTTCTTACCTTGAAA	602
DB	11821	CGAGGAGGAAATCTCGGCCATGAACCTCGATCGCAGAGCGATGTTCTTCTCTGAAA	11880
QY	603	CTATACGATTGGCCCGGAGGTAGATCATCAGATTGTCAAGGCTGATGAGTGGTGA	662
DB	11881	CTACAAGTTGGTCTGAGCTAGACCAACGATCGCCAAACCTTTCGCGCTGTCGCGA	11937
QY	663	CGCTGTTCTACGCGCGGTGAGTCAAGCTGGGCGTTCTTTCATATTCAGCCCAAGGCCAT	722

DB	11938	CGCTCACCGCACCGGCCAAGCAAGCTGGGCGTTCTTTTTCATTCACCTCCCAAGGCCCT	11997
QY	723	GTGAGAGCTCAAGGATGCTGTACCAAGACTCTTGACGCATCAACAAAGTTCTGTGTCGAC	782
DB	11998	CTCGGAGCTGAAGACGCGACCAAGACTCTTGACGCGTCTGCAAGTTGTGTCAAC	12057
QY	783	TGACGATGCTCTTTTGGGCTTCATCTGGAATTCGGGCTCTCGGTCGCTCGAAAGAT	842
DB	12058	TGATGATGCTCTTTTGGGCTTTTATCTGGCAATCAACTCGCGCTACGCTCGCAAGAT	12117
QY	843	CGATGGCTCGACCTACCGAGTTCTGCGCTGCTGTGATGCTCGACCGGCAATGGTGT	902
DB	12118	GGATGCTTCCACACTTACTGAAATTTGCGCGCTGTGCAATCTCGGGGCGCCCAATGGCGT	12177
QY	903	CTCGAACTACTACCCAGGCTTCTTCAAAACATGACTTACCAACATCGACCATCGGCGA	962
DB	12178	ATCAAGCATATACCCAGGCTTCTTCAAAACATGACTTACCAACATCGACCATCGGCGA	12237
QY	963	AATCGCAACGAGTCACTCGGCGCAACAGCATCAAGCTTCTGTTCAAGACTCGACCCCGC	1022
DB	12238	AATCGCAACGAAACCACTTGGCGCAACAGCATCAAGCTTCTGTTCAAGACTCGACCCCGC	12297
QY	1023	GAGCATGCGCCAGCAACAGAGGTCTCGGAGCTTCTCGACGCTACCTGCAACAAACCCGACA	1082
DB	12298	TCGTTTGGCGAGCAACAAAGCTTTGGCGAGCTACATGCAATGCGCTCGCTGACAAGTC	12357
QY	1083	CAACGTATCCCTGAGCGGTGATCGGACCCATCTACACGCTCATCTGAGTTCTTGGGC	1142
DB	12358	GAGCGTCTCCCTGAGCGCGATGCGAATCCGTCAGCAGCATCTGCTGAGTTCTTGGGC	12417
QY	1143	CAAGTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAAGCCGAGACTGTGAG	1202
DB	12418	CAAGTGGGACTCTGGGATTACGACTTTGGGTTTGGACTGGGTAAAGCCGAGACTGTGAG	12477
QY	1203	ACGCGCAATCTTGGGCTTGGAGCTTGGAGCTTGGATGATCTTTATGCCCAAGAGCTGATG	1262
DB	12478	AAGACTCGCTTGAACCTTTTGGAGATTGATGATCTTTATGCCCAAGAGCTGATG	12537
QY	1263	CGAGTTCTGCGCGGCTTCTCTGAGGATGAGATATGAGCCGATTTGAAGCGGATAA	1322
DB	12538	GGAGTTTACGGGCTCCATTTCTCTGAGGATGAGGATATGAGAGACTTAAGCGGATGA	12597
QY	1323	GGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG	1356
DB	12598	GGAGTGGACCAAGTACGCAAAAGTATATTTGGTTAG	12631

RESULT 6

US-10-074-279-11
; Sequence 11, Application US/10074279
; Patent No. 6646184
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 12949
; TYPE: DNA
; ORGANISM: Plasmid
US-10-074-279-11

Query Match 67.5%; Score 915.6; DB 4; Length 12949;
Best Local Similarity 80.3%; Pred. No. 46-283;
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

QY 3 GGCCTTCAAGATACAGCTCGACACCTCGGCGAGCTACAGGCTCCCTTTGATCTACAC 62
DB 11281 GTCTTTTGACATAGAGCTCGACATCATCGGCGAGCAACCGCTCTCTTTCAATCTAC 11340

QY 63 CCAATATCAGTCTCTTACCCCGTCTCTGATTCCTCAATATCCCATTTTGTGAGGAC 122
DB 11341 CAGATCATCTCTGTTTACCCCGTCTCTGATCCCTCCAGTATCCCATCGTCAGCAC 11400

QY 123 CTTTCGAGCAAGGCTTTAAGGCTTTCTCGAAGCGCTCCATGGTTCGAGGCGAGTCAA 182
DB 11401 CTTTGAAGGAGGCTTAAACGCGCTCTCTCAAACTTTCCCATGGTTCGCGGGCCAGTCAA 11460

QY 183 AGCGAGGCGCTTAGCGAGGAAACACAGGAATCTCTTTATCTGCTCCCTTTTGAAGAGCT 242
DB 11461 GACCGAGGCGCTTAGCGAGGAAACACAGGAATCTCTCAAGATCTTCCATATGAGGAGAC 11520

QY 243 TCTCTGTTGTAGTGAAGACCTCGCGATGATCTTCCAGGCGCCACGATCGAGGATAT 302
DB 11521 ACCCGCTTTGTGTGAAGACCTCGCTGATGATCTTCCAGGCGCCAAACGATCGAGGGGT 11580

QY 303 GAGAAAGCGGGATACCTATGCGATGTTTGAAGAGACATCATCGCGCCCAAGGAAGAC 362
DB 11581 GAGAAAGCGGGTTTCCCTTAGAGATGTTTGAAGAGACATCGCTCGCTCCAGGAAGAC 11640

QY 363 GTTACCTATTGACCTGTGTTACTCGTCCCGACGACCCAAAGCCCTGTAAATTTCTATTGAGCT 422
DB 11641 ATTAGCTATCGGACTTGGCAATGGCCCAACGACCCGAGGCTGTGTTGCTATTGAGCT 11700

QY 423 CAACCTTCAACGAGGCGGATCATCTCTACTGTCTCAACGAGACAGCGTGTCTATGATAT 482
DB 11701 CAACCTTCAACGAGGCGGATCATCTCTACTGTCTCAACGAGACACATGGTGTCTATGAGAT 11760

QY 483 GGTAGGCAAGATCGGCTGATCGTCTACTCTCAAGGGTGGCGTAAAGACCCATTTAC 542
DB 11761 GACAGGCAAGATCGCAATTTCTGTTCTCTCAAGGGTGGCGTAAAGACCCATTTAC 11820

QY 543 CGAAGAGGAATACGCGCCATGAACCTCGATCGCAAGAGATAGTCTCTTACCTTGAATA 602
DB 11821 CGAGGAGGAATCTCGGCCATGAACCTCGATCGCAAGAGATAGTCTCTTCTCTTGAATA 11880

QY 603 CTATACGATTTGCGCCCGAGGATGATCATCATGTTGTTCAAGCTGATGCTGTGTGA 662
DB 11881 CTACAAAGTTGGTCTGAGCTAGACACCAAGATCGCAAGAGATAGTCTCTTCTCTTGAATA 11937

QY 663 CGCTGTTCTACGCGGCTGAGTGAAGTGGGCTTCTTCAATTCAGCCCTCAAGGCCAT 722
DB 11938 CGCTCCACCCGACCGGCAAGGCAAGCTGGGCTTCTTCAATTCAGCCCTCAAGGCCAT 11997

QY 723 GTCAGAGCTCAAGGATGCTGTACCAAGCTTTTGAAGCATCAACAAAGTTGTGTGAC 782
DB 11998 CTCGAGCTGAAGAGCAGCAGCAAAAGATCTTTGAGCGCTGCTTCAAGTTTGTGTCAAC 12057

QY 783 TGAGATGCTCTTTTGGGCTTCTGGAATCGGCTCTCGGCTGCGTCTCGAAGAAAT 842
DB 12058 TGATGATGCTCTTTTGGGCTTCTGGAATCGGCTCTCGGCTGCGTCTCGAAGAAAT 12117

QY 843 CGATGGCTCTGCACCTACGAGTCTGCGGCTGCTGTTGATGCTCGACCGGCAATTTGGTGT 902
DB 12118 GGATGCTTCCACACTTACTGATTTCTGCGGCTGCTGACATGCGGGGCGCAATTTGGTGT 12177

QY 903 CTCGAACTATCCAGGCTCTTTTCAAAACATGACCTACCACTCGACCTCGAGCGGCA 962
DB 12178 ATCAAGCATATCCAGGCTCTTTTCAAAACATGACCTACCACTCGAGCGGCGGCA 12237

QY 963 AATCGCAACAGTCACTCGCGCAACAGCATCAGGCTTCTGTTTCAAGAACTTCGACCCGCG 1022
DB 12238 AATCGCAACAGTCACTCGCGCAACAGCATCAGGCTTCTGTTTCAAGAACTTCGACCCGCG 12297

QY 1023 GAGCATCGCCAGCAAGAGGTTCTCGAGCTACCTGCAACAACCCCGACAGTTC 1082
DB 12298 TCGTTTGGCGAGCAAGCAACAAGCTTTTGGCGAGTACATGCTGCGCTGCTGACAAGTC 12357

QY 1083 CAACGATATCCCTGACGGCTGATCGGACCATCTACAGGCTCATGCTGAGTTCTTTGGGC 1142
DB 12358 GAGCGTCTCCCTGACCGCGATCGAATCCGTCAAGCAGCATCATGCTGAGTTCTTTGGGC 12417

QY 1143 CAAGTGGGACTCTGGGATTAACGACTTTTGGGCTCGGACTGGGTAAAGCCGAGACTGTGAG 1202
DB 12418 CAAGTGGGATGCTGGAGTATGACTTTGGGTTGGACTGGGTAAAGCCGAGAGTGTGAG 12477

QY 1203 ACGCCCAATCTTTGAGCCTGTTGAGACTTGTGAGCTTGTATTTATGCCCAAGAGCTGTG 1262
DB 12478 AAGACCTCGCTTTGAACCTTTTGAAGTGTGATTTATTTATGCCCAAGAGCTGTG 12537

QY 1263 CGATTTCTGTCGGCGCTTTCTCTGAGGATGAGGATATGAGCGATTGAAGCGCGATAA 1322
DB 12538 GGAGTTTACCGCGCTTCAATTTCTCTGAGGATGAGGATATGAGGAGCTAAAGCGGATGA 12597

QY 1323 GGAGTGACCAAGTATGCGCAGTACGTTGGTTAG 1356
DB 12598 GGAGTGACCAAGTATGCGCAAGTATATTTGGTAG 12631

RESULT 7
US-09-538-414-10
; Sequence 10, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 13737
; TYPE: DNA
; ORGANISM: Plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
; US-09-538-414-10

Query Match 67.5%; Score 915.6; DB 3; Length 13737;
Best Local Similarity 80.3%; Pred. No. 41e-283;
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

QY 3 GGCCTTCAAGATACAGCTCGACACCTCGGCGAGCTACAGGCTCCCTTTGATCTACAC 62
DB 50 GTCTTTTGACATAGAGCTCGACATCATCGGCGAGCAACCGCTCTCTTTCAATCTACAC 109

QY 63 CCAATATCAGTCTCTTACCCCGTCTCTGATTCCTCAATATCCCATTTTGTGAGGAC 122
DB 110 CCAGATCAGTCTCTTACCCCGTCTCTGATTCCTTCCAGTATCCCATCGTCAGCAC 169

QY 123 CTTTCGAGCAAGGCTTTAAGGCTTTCTCGAAGCGCTCCCATGGTTCGAGGCGAGTCAA 182
DB 170 CTTTGAAGGCGCTTAAACGCGCTCTCTCAAACTTTCCCATGGTTCGCGGGCGAGTCAA 229

QY 183 AGCGAGGCGCTTTAGCGAGGAAACACAGGAATCTTCAAGAACTTCCATATGAGGAGAC 242
DB 230 GACCGAGGCGCTTAGCGAGGAAACACAGGAATCTTCAAGAACTTCCATATGAGGAGAC 289

QY 243 TCTCTGTTGTAGTGAAGAGCTCTCGCGATGATCTTCTGAGGCGCCACCATCGAGGATAT 302

Db 290 ACCCGCTTGTGGTGAAGACCTCGTGATGATTCCTCAGCGCCAAACGATCGAGGGGTT 349
Qy 303 GAGAAAGCGGGATACCCCTATGCGATGTTTGACGAGAAACATCATCGCGCCCAAGGAAGAC 362
Db 350 GAGAAAGCGGGTTTCCCTTAGAGATGTTTGACGAGAAACGTCGTCGCTCCGAGGAAGAC 409
Qy 363 GTTACCTATTGACCTGTGACTGTCGCCAGAGCCCAAGAGCCCTGTAATTTCTATTGCGAGCT 422
Db 410 ATTAGCTATCGGACCTGGCAATGGCCCAACGACCGCAAGCCCTGTGTTGCTATTGCGAGCT 469
Qy 423 CAACTTTCATCAGGGCGGACTCATCTCACTGTCAACGGACAGCAGCGGTCTATGGATAT 482
Db 470 CAACTTCATTAGGGCGGACTCATCTCAACGGACAGCAACATGGTGTCTATGGACAT 529
Qy 483 GGTAGGCCAAGATGCGGTGATCCGTCCTCACTGTCAACGGACAGCAGCGGTCTATGGATAT 542
Db 530 GACAGGACAAAGATGCAATTTATTTCGTCTTCTCCTCAAGGCGTCCGCAACGAAATCATTTAC 589
Qy 543 CGAAGAGGAAATGACCGCCATGAACCTCGATCGCAAGCGGTAGTCCCTCTCTCTTGAATA 602
Db 590 CGAGGAGGAAATCTCGGCCATGAACCTCGATCGCAAGCGGTAGTCCCTCTCTCTTGAATA 649
Qy 603 CTATACGATTGCGCCGAGGTAGATCATCAGATTGTCAAAGCTGATGATGCTGGTGCA 662
Db 650 CTACAAAGTTGGTCTGAGCTAGACCAACAGATCGCCAAAC---TGCCTCTGCTGGCA 706
Qy 663 CGCTGTTCTCAGCCCGGTGAGTCAAGCTGGGGTCTTTCACATTCAGGCCCAAGGCCAT 722
Db 707 CGCTCACCGCACCGGCCAAGGCAAGCTGGGGTCTTTCATTCACTCCCAAGGCCCT 766
Qy 723 GTCAGAGCTCAAGGATGCTGTACCAAGACTCTTTGACCGATCAACAAAGTTGCTGTGCA 782
Db 767 CTCGAGCTGAAAGACGACGACCAAGACTCTTGACGGGTGCTCAAGTTTGTGTCAAC 826
Qy 783 TGACGATGCTCTTTCGGGCTCATCTGGAATCGGCTCTCGCGTGGCTCGAAGAT 842
Db 827 TGATGATGCTCTTTCGGGCTTATCTGGCAATCAACCTCGCGGTACGCTCGCAAGAT 886
Qy 843 CGATGCTCTGACCTTACCGAGTTCTGCGGTGCTGTGATGCTCGACCGGCAATGGGT 902
Db 887 GATGCTTCCACACTACTGAAATCTGCGCGCTGTGACATGCGGGGCCAATGGGCT 946
Qy 903 CTCGAACAATACCCAGGCTCTTCAAAACATGACCTACCAACCTCGACCATCGGCA 962
Db 947 ATCAAGCATATACCCAGGCTCTTCAAAACATGACCTACCAACCTCGACCGTCCGCA 1006
Qy 963 AATCGCAAGGATCACTCGGCGACACGATCAGCTTCTGTCAGACTCGACCCCGC 1022
Db 1007 AATCGCAAGGACCACTTGGGCGCAACGATCAGCTCGGCTCGGAACCTCAACAGTGA 1066
Qy 1023 GAGCATGCGCCAGCGAAACAGAGGTCTCGGAGCTACCTGCAACAAACCCCGACAAATC 1082
Db 1067 TCGTTTGCAGACGAAACAGAGCTTGGGAGCTACATGCTGCTGCTGACAAATC 1126
Qy 1083 CAAAGCTATCCCTGACCGGTGATCGGACCCATCTACAGCGTATGCTGAGTTCTTGGGC 1142
Db 1127 GAGCGTCTCCCTGACCGCGGATCGGAATCGTCAAGCAGCATCATGCTGAGTTCTTGGGC 1186
Qy 1143 CAAAGTGGGACTCTGGGATTAAGACTTTGGGCTCGGACTGGGTAAAGCCCGAGCTGTGAG 1202
Db 1187 CAAAGTGGGATGCTGGGAGTATGACTTTGGGTTTGGACTGGGTAAAGCCCTGAGAGTGTGAG 1246
Qy 1203 ACGGCCAATCTTTGAGCTTTGAGAGCTTGTATCTTTATGCCCCAAGAGCTGATGG 1262
Db 1247 AAGACCTCGCTTGAACCTTTTGAAGTTTGTATGTTTATGTTTATGCCCCAAGAGCTGATGG 1306
Qy 1263 CGAGTTCTGTGCGGCTTTCTCTGAGGATGAGGATATGGAACCGATTTGAAGCGGATAA 1322
Db 1307 CGAGTTTACGGCTCCATTTCTCTGAGGATGAGGATATGGAGACTAAAGCGGATGA 1366
Qy 1323 GGAGTGACCAAGTATGCGGAGTACCTGGTTAG 1356
Db 1367 GGAGTGACCAAGTATGCGGAGTATATGGGTAG 1400

RESULT 8
US-10-074-279-10
; Sequence 10, Application US/10074279
; Patent No. 6646184
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 13737
; TYPE: DNA
; ORGANISM: Plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
US-10-074-279-10

Query Match 67.5%; Score 915.6; DB 4; Length 13737;
Best Local Similarity 80.3%; Pred. No. 4.1e-283;
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;
Qy 3 GCCTTTCAGATACAGCTCGACACCTCGGCGAGCTACAGGCTCTCTTTCGATCTACAC 62
Db 50 GTCCTTTCAGATACAGCTCGACATCATCGGCGAGCAACCGCTCTTCTTTCGATCTACAC 109
Qy 63 CCAATTCAGTCTCTCTACCCGCTCTCTGATTCCTCTCAATATCCACATATTTGTTCAGAC 122
Db 110 CCAGATCAGTCTCTGTTTACCCGCTCTCTGATCCCTCCAGTATCCACCATCGTCAGCAC 169
Qy 123 CTTGAGCAAGGCTTTAAGCGCTTCTCCGAAGCGGTCCCATGGTTCGAGGCGCAGGTCAA 182
Db 170 CTTGAGCAAGGCTTTAAGCGCTTCTCTCAAACTTCCCATGGTTCGCGGCGCAGGTCAA 229
Qy 183 AGCCGAGGCAATTAGCGGGAACACAGAACTTCTTTATCGTCCCTTTTTCGAGACGT 242
Db 230 GACCGAGGCAATCAGCGAAGGAAACACAGAACTTCCAAAGATCATTTCCATATGAGGAGAC 289
Qy 243 TCCTCGTGTGTGTAGTGAAGACCTCCGCGATGATCCTTCAGCGCCCAACGATCGAGGTTAT 302
Db 290 ACCCGCTCTTGTGTGAAGACCTCCGATGATGATTCCTCAGCGCCCAACGATCGAGGGTT 349
Qy 303 GAGAAAGCGGATACCCCTATGCGGATGTTTTCAGAGAAACATCATCGCGCCCAAGGAAGAC 362
Db 350 GAGAAAGCGGCTTTCCCTTAGAGATGTTTTCAGAGAAACGTCGTCGCTCCGAGGAGAC 409
Qy 363 GTTACTTATGACCTGTGACTGTCGCCAGCACCCCAAGCCCTGTAATTTCTATTGCGAGCT 422
Db 410 ATTAGCTATCGGACCTTGGCAATGGGCCCCAACGCCAGGCTGTGTTGCTATTGCGAGCT 469
Qy 423 CAACTTTCATCAGGGCGGACTCATCTCACTGTCAACGGACAGCAGCGGTCTATGGATAT 482
Db 470 CAACTTCATTAGGGCGGACTCATCTCAACCGTCAACGGCAACATGGTGTCTATGGACAT 529
Qy 483 GGTAGGCCAAGATGCGGTGATCCGTCCTCACTGTCAACGGCGTCCGCTTAACGCCATTTAC 542
Db 530 GACAGGACAAAGATGCAATTTATTTCGTCTTCTCCTCAAGGCGTCCGCAACGAAATCATTTAC 589
Qy 543 CGAAGGAGGAAATGACGGCCATGAACCTCGATCGCAAGAGGATGTTCTTCTTACCTTGAATA 602
Db 590 CGAGGAGGAAATCTCGGCCATGAACCTCGATCGCAAGAGGATGTTCTTCTTCTTCTTGAATA 649

603 CTATACGATTGCGCCGAGGTAGATCATCAGATTGTCAAAGTGTAGTGTGGTGA 662
Db |||||
650 CTACAAAGTTGGTCTCTAGCTAGACACACAGATGCCAAAC--TGCCTGTCTGGCGA 706
Qy |||||
663 CGCTGTTCTCAGCGGTCAGTCAAGCTTGGCGCTTCTTCAATTCAGCCCCCAAGGCCAT 722
Db |||||
707 CGCTCACCGCCAGCGCCAGCGAAGCTTGGCGCTTCTTTCATTCACCTCCCAAGGCCCT 766
Qy |||||
723 GTACAGCTCAAGGATGCTGTACCAAGACTCTTGAAGCATCAAAAGTTGCTGTGCAC 782
Db |||||
767 CTCGGAGCTGAAGACGCGACGACAAAGACTCTTGAAGCTGCTGCAAGTTTGTCTCAAC 826
Qy |||||
783 TGACGATGCTCTTTCGGCGCTTCTTGAAGTTCGGCTCTCGCGCTCTCGAAGAAAT 842
Db |||||
827 TGATGATGCTCTTTCGGCGCTTCTTGAAGTTCGGCTCTCGCGCTCTCGAAGAAAT 886
Qy |||||
843 CGATGCTCTGACCTTACCGAGTCTTGGCGCTGCTGTGATGCTCGACCGGCAATGGGT 902
Db |||||
887 GGATGCTTCAACCTACTGAAATCTGCGCGCTGTGACATGCGGGGCCAATGGGCT 946
Qy |||||
903 CTCGAACAACTACCGAGCTTCTCAAAACATGACCTACCAACACTCGACCTCGGCGA 962
Db |||||
947 ATCAAGCACAATACCGAGCTTCTTCAAAACATGACCTACCAACACTCGACCTCGGCGA 1006
Qy |||||
963 AATCGCAACGAGTCACTCGCGCAACAGCATCAGCGCTTCTGTTCAAGAACTCGACCGCG 1022
Db |||||
1007 AATCGCAACGAACTCTTGGCGCAACAGCATCAGCGCTTCTGTTCAAGAACTCGACCGCG 1066
Qy |||||
1023 GAGCATGCGCGACGCAAGAGGTCTCGAGCTACCTGCAACAAACCCCGCAAGTTC 1082
Db |||||
1067 TCGTTTGGCGAGCAACAACTTGGCGAGTACATGATGCGCTTCTGCAAGTTC 1126
Qy |||||
1083 CAAGCTATCCCTGAGCGGTGATCGGCAACCATCTACAGGGTCTGCTGAGTCTTGGCG 1142
Db |||||
1127 GAGCGTCTCCCTGACCGCGATCGAATCGTCAAGCAGCATCATGCTGAGTCTTGGCG 1186
Qy |||||
1143 CAAGTGGGACTCTGGGATTAACACTTGGGCTCGGCTGAGTAAAGCGGAGCTGTGAG 1202
Db |||||
1187 CAAGTGGGATGCTGGGAGTATGACTTGGGTTGGACTGGTAAAGCTGAGAGTGTGAG 1246
Qy |||||
1203 ACGGCCAATCTTGAAGCTTGTGAGCTTGTGAGTGTGATCTTATGCCCAAGAGCTGATGG 1262
Db |||||
1247 AAGACCTCGCTTGAACCTTTCAGAGTCTTGTGATCTTATGCCCAAGAGCTGATGG 1306
Qy |||||
1263 CGAGTCTGTCGCGCGCTTCTCTGAGGATGAGGATATGACCGGATTTGAAGCGGATAA 1322
Db |||||
1307 GGAGTTTACCGCGCTTCAATTTCTGAGGGATGAGGATATGAGAGACTAAAGCGGATGA 1366
Qy |||||
1323 GGAGTGACCAAGTATGCGCAGTACGTTGGTTAG 1356
Db |||||
1367 GGAGTGACCAAGTACGCAAGATATATTTGGGTAG 1400

RESULT 9

US-09-538-414-7

; Sequence 7, Application US/09538414

; Patent No. 6346655

; GENERAL INFORMATION:

; APPLICANT: Hohn, T.

; APPLICANT: Salmeron, J.

; APPLICANT: Peters, C.

; APPLICANT: Kendra, D.

; APPLICANT: Reinders, J.

; APPLICANT: Kuznia, R.

; APPLICANT: Dill-Mackey, R.

; TITLE OF INVENTION: Transgenic Plant and Methods

; FILE REFERENCE: sequence list

; CURRENT APPLICATION NUMBER: US/09/538,414

; CURRENT FILING DATE: 2000-03-29

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 1425

; TYPE: DNA

; ORGANISM: Saccharomyces cerevisiae

US-09-538-414-7

Query Match 18.4%; Score 249.8; DB 3; Length 1425;

Best Local Similarity 51.9%; Pred. No. 9.1e-70;

Matches 700; Conservative 0; Mismatches 622; Indels 27; Gaps 5;

Qy 16 CAGCTCCACACCCCTCGGCCAGCTACCAAGGCTCTCTTCGATCTACACCCCAATCAGTCTC 75
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Qy 64 CAATCTGATATTTGGACACAACTTCGCTATACAACTATACACTCAATATGCTCT 123
Db |||||
Qy 76 CTCTACCCCGTCTCTGATTTCTCTCAATATCCCATATTTGTCTGACACTTCGAGCAAGT 135
Db |||||
Qy 124 ATCTACCGTGTACAGATCTCTCTCTCATGACCATATCGTAAATACCTTAAACAAGAGGA 183
Qy 136 CTTAAGCGCTTCTCCGAAGCGTCCCATGGTTCGAGCCAGGTCAAAGCCGAGGCGATT 195
Db |||||
Qy 184 CTTGAAACATTTGGCTTAAATAATTTCCAGTGGCTAGCAGAAATGCTGTAATGAAGTGTCT 243
Qy 196 AGCGAGGAAACACAGGAACCTTCTCTTATCTGCTCCCTTTTGGAGGAGTTCCTCTGTTGTA 255
Db |||||
Qy 244 GACGAGGTAACACTGGTACTCAGAAATTTGTCGCTCAGACAAATTTCCAC---TTATC 300
Qy 256 GTGAAAGACCTCCCGGATGATCTTTCAGCGCCGACGATCGAGGATGAGNAAGCGCGGA 315
Db |||||
Qy 301 GTCCAAGATCTTCGAGAAGATCTGTCTGCCCAACAAATGGATTCGCTTGAAAAAGCTGAC 360
Qy 316 TACCTATGGCGATGTTTGACGAAACATCATCGCGCCCAAGGAAGAGCTT-----ACCT 369
Db |||||
Qy 361 TTTCTATCTACATGTTAGACGAAAGACTTTTTCGCGCTTGCATGACTATCAATCCACT 420
Qy 370 ATTGACCTGTGATCTGCTCCGACGACCCAAAGCTGTAAATCTTATTTGAGCTCAACTTC 429
Db |||||
Qy 421 GGAACACTATAGGTATGCGCGCAAGAGTGGGCTGTATTTGAGTTTCAAGCAAACTTT 480
Qy 430 ATCAAGGCGGACTCATCTCTCACTGTCAACGACGACGCTGTATGATATGATGATGATG 489
Db |||||
Qy 481 ATCTCCGCGCGCTCTTAACTATTTGCGGGCAGCAAAATATTTGATATTAACAGGA 540
Qy 490 CAAAGATGCGGTGATCCGCTCTACTCTCCAAGCGGTGCCGTAAACGCCCAATTCACGGAAG 549
Db |||||
Qy 541 CAGGAAAGTATCACTCACTTCTCAATAAATTTGCCACCAAAACCTTTCTCTGATGAA 600
Qy 550 GAAATGACGCGCATGAACTCGATCGAAGAGGATGTTCTCTTACCTTGAAACTATACG 609
Db |||||
Qy 601 GAACTGCTCATTTGGAATATATAGATAAAAGCAAACTATTTCTCTTTGTTGATAAACTTGG 660
Qy 610 ATT---GGCCCCGAGGTAGATCATCAGATTGTCAAGCTGATGTAGCTGGTGGTGCAGCT 666
Db |||||
Qy 661 GAAACCGACACACCGCTAGTTCATGAAATAGTGGAAACCTCTAGAAATACAACTGAGAG 720
Qy 667 GTTCTCAGCCCGGTTCAGT-----GCAAGCTGGGCTTCTTCAATTCAGCCCCCAAG 717
Db |||||
Qy 721 GAAAGGAACTCTTGTCTTCGAACTCTACTTGGGCTTATGTTGAAATTTTCTGCTATC 780
Qy 718 GCATGTCTAGACTCAAGATGCTCTCAACAGACTCTTGACGCTATCAACAAAGTTCTGTG 777
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Qy 781 TCATTGCAATCTGAGGATTTTGGCAATGCAATGATCTTCTGGGCAAAATTTGTC 840
Qy 778 TCGACTGACGATGCTCTTTTCGGCGTTTCATCTGGAATCGGCCCTCTCGGCTGCGTCTCGAA 837
Db |||||
Qy 841 TCACATGATGATCTGCTCACTGCTTTCATCTGGAATCAGTTTCTCGAGCCGCTTATCT 900
Qy 838 AGAATCGATGGCTCTGCACTACCGAGTTCCTCGCGTGTGTTGATGCTCGACCGGCAATG 897
Db |||||
Qy 901 CGACTTAAACACGAAACGAAATCAAATTTAGGCGGTCTGTGGATGTTTAGAAAAACGGCTA 960
Qy 898 GGTGCTCTGAAACAACTTACCCAGCGCTTCTTCAAAACATGACCTTACCAACTCGACCATC 957
Db |||||
Qy 961 GGACTCCCGAAACGATATCCAGGTTTATGATCAACATGACCTTTAATACAGGTTCCCTG 1020

QY 958 GGGGAAATCGCCAAACAGTCACTCGCGGCAACAGATCAAGCCCTTCGTTCAAGACTCGAC 1017
DB 1021 AAAAGCTTGGATCATAAAAGTTTGGGGCTTTGGGCTATCATAGATCAAGATTCGCGAGGAGCTAGAC 1080
QY 1018 CCGCGGAGCA-----TGGCGGAGCAACAAAGAGTCTCGCGAGTACCTGCGACACAAAC 1071
DB 1081 CCTAAAGTCTTCGATTTGGCTTAAATACATGCGCACTTGTACGCTCTTAGCCGATGC 1140
QY 1072 CCGACAAGTCCAACGTATCCCTGACGGCTGATGCGGACCCATCTACAGCGTCAATGCTG 1131
DB 1141 CCGGACAAGCAATAGGTTTCTATACCTCAACCAATTTGATCTTCAATCTGGAATTTATGGTC 1200
QY 1132 AGTTCTTGGCCNAGTGGGACTCTGGGATTAGACTTTGGGCTCGGACTGGTAAAGCCC 1191
DB 1201 AGTTCTGCGGCAAAAGTCAAGCTGTATGACGTTGATTTCAATCTAGGGCTTGGGAAAGCCC 1260
QY 1192 GAGACTGTGAGACGGCCAAATCTTTGAGCCTGTTGAGAGCTTGTATGTTTATGCCCCAAG 1251
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QY 1252 AAGCCTGATGGCGAGTTCTGTGCGGCGCTTTCTCTGAGGAGTGAAGATATGACCGATTG 1311
DB 1321 TCCTCCAGAGGTGAATGGTGTGCTCTTTGCTTTAGAGATAAAGATTTGGGAGTGCCTG 1380
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RESULT 10

US-10-074-279-7

; Sequence 7, Application US/10074279

; Patent No. 6646184

; GENERAL INFORMATION:

; APPLICANT: Hohn, T.

; APPLICANT: Salmeron, J.

; APPLICANT: Peters, C.

; APPLICANT: Kendra, D.

; APPLICANT: Reinders, J.

; APPLICANT: Kuznia, R.

; APPLICANT: Dill-Mackey, R.

; TITLE OF INVENTION: Transgenic Plant and Methods

; FILE REFERENCE: sequence list

; CURRENT APPLICATION NUMBER: US/10/074,279

; CURRENT FILING DATE: 2002-02-12

; PRIOR APPLICATION NUMBER: US/09/538,414

; PRIOR FILING DATE: 2000-03-29

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 1425

; TYPE: DNA

; ORGANISM: Saccharomyces cerevisiae

US-10-074-279-7

Query Match 18.4%; Score 249.8; DB 4; Length 1425;
Best Local Similarity 51.9%; Pred.No. 9.1e-70;
Matches 700; Conservative 0; Mismatches 622; Indels 27; Gaps 5;

QY 16 CAGCTCGACACCTCGCCAGCTACCAAGGCTCTTCGATCTACACCCAAATCAGTCTC 75
DB 64 CAACCTTGATATTTTGGGCAACAACCTTCGCTATACAAAATACACTCAAAATATGCTCT 123
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DB 184 CTTGAACATTGCTATAAAATTTCCAGTGGCTAGCAGGAAATGTCGTAATGAAGTGCT 243
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DB 244 GAGGAAGGTAAACACTGGTACCTACAGAAATTTGCCCTCAGACAAAATTCAC-----TTATC 300
QY 256 GTGAAAGACTTCGCGATGATCTTTCAGCGCCCCAGATCAGGGGTATGAGAAAGCGGGA 315
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QY 316 TACCTTATGGCGATGTTTTCAGGAGAATCATCGCGCCCAAGGAGACGTT-----ACCT 369
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QY 490 CAAGATGCGGTGATCGGTCTACTCTCCAAGGCGTGCCTAACGACCCATTCACGGAAGAG 549
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DB 781 TCATTGCAAAATCTGAGGATTTTGGCAATGCGAGACATGACTTCTGGCACAATAATTTGTC 840
QY 778 TCGACTGACGATGCTCTTTTCGGCGTTTCATCTGGAATCGGCCCTCTCGCGTCTCGAA 837
DB 841 TCCACTGATGATATCGTCACTGCTTTCATCTGGAATCAGTTTCTCGAGCCGCTTATCT 900
QY 838 AGAATCGATGGCTCTGACACTACCGAGTCTCGCGTCTGTTGATGCTCGACCGGCAATG 897
DB 901 CGACTTAAACCCAGAAAACGAAATCAAATTTAGGCGGTGCTGTGGATGTTAGAAAACGGCTA 960
QY 898 GTGTCTCGAACAACCTACCCAGGCTTCTTCAAACATGACCTTACCACAACTCGACCATC 957
DB 961 GGACTCCCCGAAACGATTCAGGGTTATTAGTCAACATGACCTTTTAAATACAGGTTCCCTG 1020
QY 958 GCGAAATCGCAACGAGTCACTCGGCGCAACAGCATCAAGCTTCGTTTCAGAACTCGAC 1017
DB 1021 AAAAGCTTGGATCATAAAAGTTTGGGCGTTCTTGATCATCAGATTCGAGGAAGCTAGAC 1080
QY 1018 CCGCGAGCA-----TGGCGGAGCAACAAGAGTCTCGGAGCTACCTGCAACAAC 1071
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; LENGTH: 720
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-16032

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	Best Local Similarity	53.3%	Pred. No.	1.1;						
	Matches	72;	Conservative	0;	Mismatches	63;	Indels	0;	Gaps	0;
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Db	244	TATGATCTCTGGAAGCCAGCAGGCGCTGCTTCGGCATCTCGCCGAGACAGCCAGGAAGCT	303							
Qy	534	CCCATTCACCGAAGAGAAATGACGGCCATGAACCTCGATCGGAAGACGATAGTTCCTTAA	593							
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US-09-252-991A-16568/c
; Sequence 16568, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

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	Query Match	2.5%; Score 34.2; DB 4; Length 1074;	
	Best Local Similarity 53.3%; Pred. No. 1.4;		
	Matches 72; Conservative 0; Mismatches 63; Indels 0; Gaps 0;		
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Db	864	TATGATGCTGGAAGACGACGAGGCGTGCTTCGGCATCTCGCGAGACGCCAGGAGCT	805
Qy	534	CCCATTCAACCGAAGAGAAATGACGGCCATGAACTTCGATCGCAAGACGATAGTTCCTTA	593
Db	804	CACCATCACCTCGACARGATGATGGTCATCAGCAACAGGTACGCCATCTGCCACGTC	745
Qy	594	CCTTGAACAACCTATAC	608

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 23, 2005, 04:49:05 ; Search time 4735 Seconds
(without alignments)
10435.539 Million cell updates/sec

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Perfect score: 1356
Sequence: 1 atgggtttcaagatacagct.....atgcgcagctacgttggttag 1356

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	406	29.9	1055	4	BI947129
3	354.2	26.1	512	4	BI191800
4	351	25.9	508	4	BI191865
5	323.4	23.8	498	4	BI200717
C 6	317.6	23.4	499	4	BI191678
C 7	296.6	21.9	481	4	BI191864
8	278.4	20.5	514	4	BI192008
9	278	20.5	411	4	BI187781
C 10	273.4	20.2	448	4	BI201068
C 11	273	20.1	518	4	BI191997
C 12	268.4	19.8	457	4	BI187780
C 13	258	19.0	392	4	BI192452
C 14	254.8	18.8	423	4	BI192458
C 15	251.2	18.5	490	4	BI201353
C 16	247.4	18.2	374	4	BI187896
C 17	242.8	17.9	476	4	BI192381
C 18	234.4	17.3	401	4	BI188598
C 19	234.4	17.3	401	4	BI192451
C 20	233.4	17.2	348	4	BI191129
C 21	231.6	17.1	459	4	BI187539
C 22	231.2	17.1	333	4	BI188605
C 23	226.6	16.7	372	4	BI192380
C 24	223.8	16.5	336	4	BI191040

C 25	218.6	16.1	358	4	BI201146
C 26	217.2	16.0	435	4	BI187304
C 27	215.4	15.9	350	4	BI190499
C 28	206.6	15.2	330	4	BI191128
C 29	202	14.9	546	2	BF253868
C 30	196	14.5	385	4	BI189867
C 31	195	14.4	318	4	BI192335
C 32	187.6	13.8	303	4	BI188705
C 33	187.6	13.8	303	4	BI189964
C 34	187.6	13.8	304	4	BI190847
C 35	187.6	13.8	308	4	BI188363
C 36	187.6	13.8	308	4	BI190145
C 37	187	13.8	311	4	BI200611
C 38	170.4	12.6	373	4	BI190862
C 39	170.4	12.6	376	4	BI189442
C 40	170.4	12.6	380	4	BI190409
C 41	169.4	12.5	352	4	BI188631
C 42	169.4	12.5	352	4	BI201565
C 43	169.4	12.5	360	4	BI187939
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
BI949616 899 bp mRNA linear EST 19-OCT-2001
HVSME10014017f Hordeum vulgare spike EST library HVCDNA0012
(Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone
HVSME10014017f, mRNA sequence.
ACCESSION
BI949616
VERSION
BI949616.1 GI:16291032
KEYWORDS
EST.
SOURCE
Hordeum vulgare subsp. vulgare
ORGANISM
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE
1 (bases 1 to 899)
Wing, R., Muehlbauer, G.J., Close, T.J., Kleinhofs, A., Wise, R.,
Heinen, S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M.,
Rambo, T., Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W.,
Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Fusarium infected Morex spike cDNA library
Unpublished (2001)
Contact: Wing RA
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 598
Seq primer: AATTAACCTCTACTAAAGG
High quality sequence stop: 755.

JOURNAL
COMMENT
Unpublished (2001)
Contact: Wing RA
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 598
Seq primer: AATTAACCTCTACTAAAGG
High quality sequence stop: 755.
FEATURES
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/mol_type="mRNA"
/cultivar="Morex"
/sub_species="vulgare"
/db_xref="taxon:112509"
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/tissue_type="Spike"
/lab_host="TJC121"
/clone_lib="Hordeum vulgare spike EST library HVCDNA0012
(Fusarium infected)"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Plants were grown at the University of Minnesota in
the GJ Muehlbauer lab; spikes were harvested and snap

frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)

ORIGIN

Query Match 49.0%; Score 663.8; DB 4; Length 899;
Best Local Similarity 95.8%; Pred. No. 2.9e-184;
Matches 724; Conservative 0; Mismatches 28; Indels 4; Gaps 4;

QY 1 ATGCTTTCAAGATACAGCTCGACACCTCGCGCAGCTACAGGCTCCTTTGATCTAC 60
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QY 61 ACCCAATCATGCTCTCTACCCCGTCTGTGATCTCTCAATATCCCACTATTGTTCAGC 120
DB 170 ACCCAATCATGCTCTCTACCCCGTCTGTGATCTCTCAATATCCCACTATTGTTCAGC 229
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RESULT 2

B1947129

LOCUS

B1947129

DEFINITION

B1947129

ACCESSION

B1947129

VERSION

B1947129.1

KEYWORDS

EST.

SOURCE

Hordeum vulgare subsp. vulgare

ORGANISM

Hordeum vulgare subsp. vulgare

REFERENCE

1 (bases 1 to 1055)

AUTHORS

Wing, R., Muehlbauer, G.J., Close, T.J., Kleinhofs, A., Wise, R., Heinen, S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W., Oates, R. and Main, D.

TITLE

Development of a genetically and physically anchored EST resource for barley genomics: Fusarium infected Morex spike cDNA library

JOURNAL

Unpublished (2001)

COMMENT

Contact: Wing R

Clemson University

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: wing@clemson.edu

Total hq bases = 147

Seq primer: AATTAACTCTCACTAAAGGG

High quality sequence start: 5

High quality sequence stop: 668.

Location/Qualifiers

1..1055

/organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"

/cultivar="Morex"

/sub_species="vulgare"

/db_xref="taxon:112509"

/clone="HVSME10003N10f"

/tissue_type="Spike"

/lab_host="TJCI121"

/clone_lib="Hordeum vulgare spike EST library HVCDNA0012 (Fusarium infected)"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Plants were grown at the University of Minnesota in the GJ Muehlbauer lab; spikes were harvested and snap frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library

preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)

ORIGIN

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Query Match      29.9%; Score 406; DB 4; Length 1055;
Best Local Similarity 79.4%; Pred. No. 3.9e-108;
Matches 481; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

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DB 121 TCTACTCTCAAGCGCTGCCGTAACGACCCATTACCGAAGAGGAAATGACGGCCATGAA 180
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QY 807 CTGGAATCGGCTCTCGGCTGCTCGACCGCAATGCGTGTGCTGACGATGCTCTTACCGAGTT 866
DB 421 CTTGGAATAGGCTCTACGGCGCTTCCAAATAATGCAAGTTCCTCCCTACCGAGTTC 480
QY 867 CTGCGTGTGTTGATGCTCGACCGCAATGGTGTGCTGAACTACCGAGGCTTCCT 926
DB 481 GCAGCTCATTTAAAGCTACACCGGCGAGGTGAGTACCAAGCAATCCAACTTAGCC 540
QY 927 TCAAAACATGACCTTACCAACTCGACCATCGGCGAAATCGCCAAAGAGTCACTCGGCGC 986
DB 541 TCGGTGAACACGCTTTCCAAACGTAAACCGCGCAACGGCATCGTGTCTCGCGGGA 600
QY 987 AACAGC 992
DB 601 ACCAGC 606
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RESULT 3

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BI191800
LOCUS      512 bp mRNA linear EST 10-JUL-2001
DEFINITION Bi191800.1 GI:14665479
            library Fusarium sporotrichioides Tri 10 overexpressed cDNA
            sequence.
ACCESSION Bi191800
VERSION   Bi191800.1
KEYWORDS  EST.
SOURCE    Fusarium sporotrichioides
           Fusarium sporotrichioides
ORGANISM  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
           Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE 1 (bases 1 to 512)
AUTHORS   Ren.Q., Tag.A., Peglow.A., Lai.H., Kupfer.C., Peterson.A.,
```

TITLE
JOURNAL
COMMENT

Beremand, M. and Roe, B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
Other ESTs: 12f1ifs.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability. Included
is the best homolog from a blastx search of Genbank nr 04-09-01
871 8e-94 gi|4379882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: T3
High quality sequence stop: 476.
FEATURES
source
1..512
/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"

ORIGIN

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Query Match      26.1%; Score 354.2; DB 4; Length 512;
Best Local Similarity 82.2%; Pred. No. 6.3e-93;
Matches 407; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 3 GGCCTTCAAGATACAGCTCGACACCTCGGCAGCTACCAAGCCCTCTTTGATCTACAC 62
DB 16 GTCTTTGACATAGAGCTCGACATCATCGCCAGCAACCGCCTCTTTTCACTACAC 75
QY 63 CCAATCAGTCTCTACCCGCTCTGATTCCTCAATATCCACATATGTCAGCAC 122
DB 76 CCAGATCAGTCTGCTTACCCGCTCTGATCCCTCCAGTATCCACCATGTCAGCAC 135
QY 123 CTTTCAGCAAGGCTTTAAGCGCTTCTCCGAAGCCGCTCCATCGGTCGAGGCCAGGTCAA 182
DB 136 CTTGAGGAGGCTTAAAGCGCTCTCTCAAACCTTCCATGGTCGCGGCCAGGTCAA 195
QY 183 AGCCGAGGCGATTAGCGAGGAAACACAGGAACCTCTCTTTATCGTCCCTTTTGAGACGT 242
DB 196 GACCGAGGCGATCAGCGAAGAAACACAGGAACCTTCCAAAGATCATTCATATGAGGAGAC 255
QY 243 TCCTCGTGTGTAGTGAAGACCTCGCATCATCTTCAGCGCCCAACCATCGAGGGTAT 302
DB 256 ACCCGGTCTTGTGGTGAAGACCTCGGTGATGATTCCTCAGCGCCCAACCATCGAGGGT 315
QY 303 GAGAAAGCGCGATACCCCTATGCGCATGTTTTCAGAGAAACATCATCGCCCAAGGAAGAC 362
DB 316 GAGAAAGCGGGTTCCTTCCCTTAGAGATGTTTGAAGAGACGTCGTCGTCGAGGAAGAC 375
QY 363 GTTACTATTGACCTGTGTAATCTGTCGCCGACGCCAAGCCCTGTAATCTTATGACGT 422
DB 376 ATTAGTATCGGACCTGGCAATGGCCCCAACGACCCGAGACCTGTGTGTTATGACGT 435
QY 423 CAACTTCATCAGGCGGACTCATCTCACTCTCAACGACGACGAGTGTGCTATGATAT 482
DB 436 CAACTTCATCAGGCGGACTCATCTCACTCTCAACGACGACGAGTGTGCTATGATAT 495
QY 483 GGTAGGCCAAGATGC 497
DB 496 GACAGGACCAAGATGC 510
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Db	313	GAGAAAGCGGGTTTCCCTTAGAGATGTTTGTGACGAAACGTGCTGCTCCGAGGAAGAC	372
Qy	363	GTATACCTATTGGACCTGCTACCTCCGACGACCCAAAGCCTGTAATTTCTATTGCGAGCT	422
Db	373	ATTAGCTATCGGACCTGGCAATGCCCAACGACCCGAGCCTGTGTGCTATTGCGAGCT	432
Qy	423	CAACTTCATCAAGGCGGACTCATCTCTCACTGTCAACGACAGACCGTGTCTATGGATAT	482
Db	433	CAACTTCATTAAGGCGGACTCATCTCTCACTGTCAACGACAGACCGTGTCTATGGACAT	492
Qy	483	GGTAGGCGCAAGATCC	497
Db	493	GACAGGCAAGATGC	507
RESULT 5			
LOCUS	BI200717	498 bp mRNA linear	EST 10-JUL-2001
DEFINITION	ole06fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone ole06fs 5', mRNA sequence.		
ACCESSION	BI200717	GI:14666689	
VERSION	1		
KEYWORDS	Fusarium sporotrichioides		
SOURCE	Fusarium sporotrichioides		
ORGANISM	Fusarium sporotrichioides		
REFERENCE	1 (bases 1 to 498)		
AUTHORS	Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand,M. and Roe,B.		
TITLE	Analysis of a Fusarium sporotrichioides EST database		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA Tel: 405 325 4912 Fax: 405 325 7762 Email: broe@ou.edu Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 857 3e-92 gi 4378882 gb AAD197 (AF127176) trichothecenes-3-O-acetyltransferase Seq primer: T3 High quality sequence stop: 476. Location/Qualifiers 1..508 /organism="Fusarium sporotrichioides" /mol_type="mRNA" /strain="Tri 10" /db_xref="taxon:5514" /clone="13b10fs" /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library" /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript"		
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ORIGIN			
Query Match	25.9%;	Score 351; DB 4; Length 508;	
Best Local Similarity	81.8%;	Pred. No. 5.6e-92;	
Matches	405; Conservative	0; Mismatches 90; Indels 0; Gaps 0;	
Qy	3	GGCTTTCAAGATACAGCTCGACACCTCGCCAGCTACAGGCTCTCTTCGATCTACAC	62
Db	13	GTCTTTTGACATAGAGCTGACATCATCGGCCAGCAACCCGCTCTCTTTCAATCTACAC	72
Qy	63	CCAAATCAGTCTCTCTACCCCGCTCTGATTCCTCTCAATATCCCACTATTGTCAGCAC	122
Db	73	CCAGATAGTCTCTTTTACCCCGTCTGATCCCTCCAGTATCCCACTATGTCAGCAC	132
Qy	123	CTTCGAGCAAGGCTTTAAGCGCTTCTCCGAAGCGCTCCCATGGTCCGAGCCAGGTCAA	182
Db	133	CTTTGAGGAGGCTTAAACCGCTCTGTCAACCTTCCCATGGTCCGCGGCGAGGTCAA	192
Qy	183	AGCCGAGGCGATTAGCGAGGAAACACAGGAACCTTCTTTATCTCTCTTTTGGAGGAGT	242
Db	193	GACCGAGGCGATCAGGAGGAGACACAGGAACCTTCCAGATCATTCATATGAGGAGAC	252
Qy	243	TCCTCGTGTGTAGTGAAGACCTCCGCGATGATCTCTTCAGCGCCACGATTCGAGGGTAT	302
Db	253	ACCCGCTCTTGTGTGAAGACCTCCGCGATGATCTCTTCAGCGCCACGATTCGAGGGGTT	312
Qy	303	GAGAAAGCGGATACCTTATGGCGATGTTTGGAGGAACATCATCGCGCCCAAGAGAC	362

QY 563 TGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAAAACTATACGATTGGCCCGGAGG 622
 Db 121 TGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAAAACTATACGATTGGCTCTGAGC 180
 QY 623 TAGATCATCAGATTGTCAAAAGCTGATGAGTGTGCTGACGCTGTCTTCACGCGGTCA 682
 Db 181 TAGACCAACAGATCGCAAAACC---TGGCGCTGCTGGGACGCTCCACCGGACCGGCCA 237
 QY 683 GTGCAAGCTGGGGCTTCTTCAATTCAGCCGCCCATGTGTCAGAGCTCAAGGATGCTG 742
 Db 238 AGCAAGCTGGGGCTTCTTCAATTCAGCTCCCAAGGCCCTCTCGGAGCTGAAAGACGAG 297
 QY 743 CTACCAAGACTCTTGACGATCAACAAAGTGTGTCGATGACGATGCTCTTTGGCGT 802
 Db 298 CCACAAGACTCTTGACGCTGCTCAAGTGTGTGTCGATGATGCTCTTTGGCGT 357
 QY 803 TCATCTGGAATCGGGCTCTCGGGTGGCTCGAAAGATCGATGCTCTGACCTPACG 862
 Db 358 TTATCTGGCAATCAACTCGCGGTGAGTCTGCAAGATGGATGTTTCCACACTACTG 417
 QY 863 AGTTCTGCGTGTGTGATGCTCGACGGCCCAATGGGTGTCTCGAACTACCCAGGCC 922
 Db 418 AATTCTGCGCGTGTGATGCTCGACATGCGGGCCCAATGGGTGTATCAACGACATACCCAGGCC 477
 QY 923 TTCTTCAAAACATGACTACC 943
 Db 478 TTCTTCAAAACATGACTACC 498

RESULT 6

BI191678/c
 LOCUS
 DEFINITION
 library f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
 library Fusarium sporotrichioides cDNA clone l11f1e 3', mRNA
 sequence.

ACCESSION
 VERSION
 KEYWORDS

SOURCE
 ORGANISM

Fusarium sporotrichioides
 Fusarium sporotrichioides
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 1 (bases 1 to 499)

Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
 Beremand,M. and Roe,B.
 Analysis of a Fusarium
 Unpublished (2001)

CONTACT: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Department of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma

620 Parrington Oval, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability Included

is the best homolog from a blastx search of Genbank nr 04-09-01

796 5e-85 gi|4378882|gb|AAD197 (AF127176)

trichothecene3-O-acetyltransfer

Seq primer: M13-20

High quality sequence stop: 428.

Location/Qualifiers

1. .499

/organism="Fusarium sporotrichioides"

/mol_type="mRNA"

/strain="Tri 10"

/db_xref="taxon:5514"

/clone="l11f1e"

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cDNA library"

/note="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2:

XhoI; 5' end of cDNA cloned into EcoRI site of

pBlueScript; 3' end of cDNA cloned into XhoI site of

pBlueScript"

FEATURES
 source

ORIGIN

Query Match 23.4%; Score 317.6; DB 4; Length 499;
 Best Local Similarity 80.7%; Pred. No. 4e-82;
 Matches 371; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
 QY 897 GGGTGTCTCGAACACTACCCAGGCTTCTTCAAAACATGACTACCACTCGACCAT 956
 Db 499 GGGCGGTATCAAGCACAATACCCAGGCTTCTTCAAAACATGACTACCACTCGACCAT 440
 QY 957 CGCGCAAAATCGCAACAGTCACTCGGCGCAACAGCATCACGCTTCTGTTTCAAACTCGA 1016
 Db 439 CCGCGAAATCGCAACAGTCACTCGGCGCAACAGCATCACGCTTCTGTTTCAAACTCGA 380
 QY 1017 CCGCGCAATCGCAACAGTCACTCGGCGCAACAGCATCACGCTTCTGTTTCAAACTCGA 1076
 Db 379 CAGTGATGTTTGGCAGACGAACAAGCTTTGGCGACGTACATGCTGCTGCTGA 320
 QY 1077 CAACTCAACGATGCTCGTACGCGGTGATCGGACCCATCTACAGGCTCATGCTGATTC 1136
 Db 319 CAACTCAACGATGCTCGTACGCGGTGATCGGACCCATCTACAGGCTCATGCTGATTC 260
 QY 1137 TTGGGCGCAAGTGGGACTCTGGGATTTACGACTTTGGGCTCGGCTAAGCCCGAGAC 1196
 Db 259 CTGGGCGCAAGTGGGATGCTGGGATGATGACTTTGGGTTTGGACTGGGTAAGCTGAGAG 200
 QY 1197 TGTGAGACGGCCCAATCTTTGAGCTGTTGAGAGCTTTGATGTACTTTATGCCCAAGAGCC 1256
 Db 199 TGTGAGAGACCTCGCTTTGAACCTTTTGAGAGTTTGTATGTTATGCCCAAGAGCC 140
 QY 1257 TGATGGGAGTCTGTGGCGCTTCTCTGAGGATGAGGATATGGACCGATTGAAGGC 1316
 Db 139 TGATGGGAGTCTGTGGCGCTTCTCTGAGGATGAGGATATGGACCGATTGAAGGC 80
 QY 1317 GATAGGAGTGGCAAGTATGCGCAGTACCTTGGTTAG 1356
 Db 79 GGATGAGGAGTGGCAAGTATGCGCAGTATGTTGGTTAG 40

RESULT 7

BI191864/c

LOCUS

DEFINITION

library f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Fusarium sporotrichioides

Fusarium sporotrichioides

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

1 (bases 1 to 481)

Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,

Beremand,M. and Roe,B.

Analysis of a Fusarium

Unpublished (2001)

Other ESTs: l3b10fs.r1

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Department of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma

620 Parrington Oval, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability Included

is the best homolog from a blastx search of Genbank nr 04-09-01

745 4e-79 gi|4378882|gb|AAD197 (AF127176)

trichothecene3-O-acetyltransfer

Seq primer: M13-20

High quality sequence stop: 340.

Location/Qualifiers

1. .481

FEATURES
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/organism="Fusarium sporotrichioides"

/mol_type="mRNA"

/strain="Tri 10"

/db_xref="taxon:5514"

/clone="13bi0fs"

/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"

/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:

XhoI; 5' end of cDNA cloned into EcoRI site of

pBluescript; 3' end of cDNA cloned into XhoI site of

pBluescript"

ORIGIN

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Query Match      21.9%; Score 296.6; DB 4; Length 481;
Best Local Similarity 80.5%; Pred. No. 6.3e-76; Indels 0; Gaps 0;
Matches 347; Conservative 0; Mismatches 84;

QY 926 TTCAAAACATGACCTACCAAACTGACCATCGGCGAAATCCCAACGAGTCACATCGCGG 985
DB 481 TTCAAAACATGACCTACCAAACTGACCATCGGCGAAATCCCAACGAGTCACATCGCGG 422
QY 986 CAACAGCATCAGCCTTGTGAACTCGACCCCGGAGCATGGCCAGCGAAACAAGAG 1045
DB 421 CAACAGCATCAGCCTTGTGAACTCGACCCCGGAGCATGGCCAGCGAAACAAGAG 362
QY 1046 GTCTCGGAGCTACCTGCAACAAACCCGCAAGTCCCAACGTCATCCCTGACGGCTGATG 1105
DB 361 CTTTGGCGAGCTACATGCAATGGCTGCTGACAGTCGAGCTCTCCCTGACCGCGGATG 302
QY 1106 CGACCCATCTTACAGCGTCATGCTGAGTTCTTGGGCCAAGTGGGACTCTGGGATTAG 1165
DB 301 CGAATCCGTCACGACGATCATGCTGAGTTCTTGGGCCAAGTGGGATGCTGGGAGTAG 242
QY 1166 ACTTTGGGCTCGAGCTGGTAAGCCCGAGACTGTGAGACGGCAATCTTTGAGCCTGTG 1225
DB 241 ACTTTGGGTTTGGACTGGTAAAGCCCTGAGAGTGTGAGAGACTCTGCTTTGAACTTTTG 182
QY 1226 AGAGCTTGATGTAATTTATGCCAAGAGCCTGATGGCGAGTTCTGTGGGGCTTTCTC 1285
DB 181 AGAGTTTGATGTAATTTATGCCAAGAGCCTGATGGCGAGTTTACGGCGTCCATTTCT 122
QY 1286 TGAGGGATGAGGATATGAGCCGATTAAGCCGATTAAGGCGGATAGGAGTGGACCAAGTATGCGCA 1345
DB 121 TGAGGGATGAGGATATGAGGAGACTAAAGCCGATGAGGAGTGGACCAAGTATGCGCA 62
QY 1346 ACCTTGGTTAG 1356
DB 61 ATATTGGGTAG 51

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RESULT 8
BI192008      514 bp mRNA linear EST 10-JUL-2001
LOCUS        14c09fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION   library Fusarium sporotrichioides cDNA clone 14c09fs 5', mRNA
sequence.
VERSION      BI192008.1 GI:14665687
KEYWORDS     Fusarium sporotrichioides
SOURCE       Fusarium sporotrichioides
ORGANISM     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
              Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
              1 (bases 1 to 514)
REFERENCE    Ren,Q., Tag,A., Pellow,A., Lai,H., Kupfer,C., Peterson,A.,
              Beremand,M. and Roe,B.
              Analysis of a Fusarium sporotrichioides EST database
              Unpublished (2001)
TITLE       Department of Chemistry and Biochemistry
JOURNAL     Advanced Center for Genome Technology, University of Oklahoma
COMMENT     620 Parrington Oval, Norman, OK 73019, USA
              Tel: 405 325 4912

```

Fax: 405 325 7762
 Email: broe@ou.edu
 Contact Dr. Marian Beremand regarding clone availability Included
 is the best homolog from a blastx search of Genbank nr 04-09-01
 730 3e-77 gi|4378882|gb|AAD197 (AF127176)
 trichothecene3-O-acetyltransfer
 Seq primer: T3
 High quality sequence stop: 476.

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Location/Qualifiers
/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="14c09fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"

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ORIGIN

```

Query Match      20.5%; Score 278.4; DB 4; Length 514;
Best Local Similarity 81.0%; Pred. No. 1.5e-70; Indels 0; Gaps 0;
Matches 324; Conservative 0; Mismatches 76;

QY 3 GGCTTTCAAGATACAGCTCGACACCCCTCGGCCAGCTACCGAGCCTCTTTTCGATCTACAC 62
DB 115 GTCITTTGACATAGAGCTCGACATCATCGGCCAGCAACCGCCTCTTCTTCAATCTACAC 174
QY 63 CCAATCATGCTCTCTTACCCCGCTCTGATCTCTCTCAATATCCCATATGTCAGCAC 122
DB 175 CCAGATCATGCTCGCTTTACCCCGCTCTGATCTCTCTCCAGTATCCCACTCGTCAGCAC 234
QY 123 CTTTCGAGCAAGGTCTTAAGCGCTCTTCGAAAGCGTCCCATGGGTGCGAGCCAGGTCAA 182
DB 235 CTTGAGGAAGCGCTTAAACCGCTCTCTCAAACTTCCATGGGTGCGGGCCAGGTCAA 294
QY 183 AGCCGAGGCGCATTAGCGAGGGAACACAGGAACCTCTTTATCGTCCTTTTGAGGAGCT 242
DB 295 GACCGAGGCGCATCAGCGAAGGAACACAGGAACCTTCCAAAGATCATTCATATGAGGAGAC 354
QY 243 TCCTCGTGTGTAGTGAAGACCTCCGCGATGATCTTCAGCGCCCGACGATCGAGGTAT 302
DB 355 ACCCGCTCTGTGTGGAAGACCTCCGTCGATGATTCCTCAGCGCCCAAGATCGAGGGTT 414
QY 303 GAGAAAGCGGGATACCCCTATGGCGATGTTTGACGAGAACATCATCGCGCCCAAGGAAGAC 362
DB 415 GAGAAAGCGGGTTCCTCTTAGAGATGTTTGACGAGAACGTCGTCGTCGCGAGGAAGAC 474
QY 363 GTTACCTATTGACCTGTGTACTGTGTCCTCGAGACGCCCAAG 402
DB 475 ATTAGCTATGACCTGTGCAATGGCCCAAGACGCCCGAAG 514

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RESULT 9
BI187781      411 bp mRNA linear EST 10-JUL-2001
LOCUS        b2d04fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION   library Fusarium sporotrichioides cDNA clone b2d04fs 5', mRNA
sequence.
VERSION      BI187781
KEYWORDS     Fusarium sporotrichioides
SOURCE       Fusarium sporotrichioides
ORGANISM     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
              Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
              1 (bases 1 to 411)
REFERENCE    Ren,Q., Tag,A., Pellow,A., Lai,H., Kupfer,C., Peterson,A.,
              Beremand,M. and Roe,B.
              Analysis of a Fusarium sporotrichioides EST database

```

JOURNAL Unpublished (2001)
COMMENT Other ESTs: b2040fs.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
591 4e-61 gi|4378882|gb|AAD197 (AF127176)
trichothecenes3-O-acetyltransfer
Seq primer: T3
High quality sequence stop: 307.
Location/Qualifiers
1. .411
/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="b2040fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/notes="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"

ORGANISM Fusarium sporotrichioides
REFERENCE 1 (bases 1 to 448)
AUTHORS Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A.,
Beremand, M. and Roe, B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
594 4e-73 gi|4378882|gb|AAD197 (AF127176)
trichothecenes3-O-acetyltransfer
Seq primer: M13-20
High quality sequence stop: 303.
Location/Qualifiers
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cDNA library"
/notes="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"

FEATURES
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1. .448
/organism="Fusarium sporotrichioides"
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cDNA library"
/notes="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"

ORIGIN
Query Match 20.5%; Score 278; DB 4; Length 411;
Best Local Similarity 81.2%; Pred. No. 1.9e-70;
Matches 336; Conservative 0; Mismatches 75; Indels 3; Gaps 1;
QY 401 AGCGTGAATTCATTCAGCTCAATCTATCAAGGCGGAGCTCATCTCAGTCAACG 460
DB 1 AGCGTGTGTTGCTATTGAGCTCAATCTTCAATTAAGGCGGAGCTCATCTCAGGCTCAACG 60
QY 461 GACAGCAGGTGCTATGGATATGATGGTATAGGCAAGATCGGTGATCGCTACTCTCCAAGG 520
DB 61 GACAACTGTTGCTATGGACATGACAGGACAAAGATGCAATTATTCGTTCTCTCCAAGG 120
QY 521 CGTCCGTAAACGACCAATTCACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGA 580
DB 121 CGTCCGCAACGAATCATTCACCGAGGAGAAATCTCGGCCATGAACCTCGATCGCAAGA 180
QY 581 CGATAGTCTCTTACCTTGAACCTATACGATTCGCCCGGAGGTAGATCATCATGATGTCA 640
DB 181 CGGTAGTCCCTCTCTTTGAAACTACAAAGTTGGTCTTGAGCTAGACCCAGATCGCCA 240
QY 641 AAGCTGATGTAGTGTGTGTGAGCTGTTCTCACGCCGGTCACTGCAAGCTGGGCGTTCT 700
DB 241 AACC--TGCGCTGTGGGAGCGCTCCACCGCA CGGCCAAGGCAAGCTGGGCGTTCT 297
QY 701 TCATATTACGCCCAAGGCAATGTCAAGCTCAAGATGCTGTAACAAGACTCTTTGACG 760
DB 298 TTTCAATTAATCTCCCAAGGCGCTCTCGAGCTGAAAGACGAGCCACAAAGACTCTTTGACG 357
QY 761 CATCAACAAGTTCGTGTGCTGATGATGCTCTTTTCGGGTTTCATCTGGAAT 814
DB 358 CGTCGTCGAAGTTGTGTAACGTGATGCTCTTTTCGGGTTTATCTGGCAAT 411

RESULT 10
BI201068/c 448 bp mRNA linear EST 10-JUL-2001
LOCUS o4c12fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION library Fusarium sporotrichioides cDNA clone o4c12fs 3', mRNA
sequence.
ACCESSION BI201068
VERSION BI201068.1 GI:14667040
KEYWORDS EST.
SOURCE Fusarium sporotrichioides

ORIGIN
Query Match 20.2%; Score 273.4; DB 4; Length 448;
Best Local Similarity 79.9%; Pred. No. 4.4e-69;
Matches 322; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY 954 CATCGCGAAATCGCCACGAGTCACTCGCGCAACAGCATCAGCGCTTCGTTTCAGAACT 1013
DB 448 CGTTCGCGAAATCGCCACAAACCACTTCGCGCAACAGCATCAGCGCTTCGTTTCAGAACT 389
QY 1014 CGACCCCGCGAGATGCGCCAGCAACAAGAGTCTCTCGGACGTACTCGCACAAACCC 1073
DB 388 CAACAGTGATGTTTGGCGAGACGACACAAGCTTTGGCGAGCTACATGATGCTGCC 329
QY 1074 CGACAAGTCCACGTATCCCTGACGGCTGATGGGACCCATCTACAGGTCATGCTGAG 1133
DB 328 TGACAAGTCGAGCGTCTCCCTGACCGCCGATCGAATCGGTCAAGCAGCATCATGCTGAG 269
QY 1134 TTCTTGGGCAAGTGGGACTCTGGGATTTACGACTTTGGGCTGGGCTGGTAAGCCGA 1193
DB 268 TTCTTGGGCAAGTGGGATGCTGGGAGTATGACTTTGGGTTTGGACTGGGTAAAGCTGA 209
QY 1194 GACTGTGAGACGCGCCAAATCTTTGAGCCTGTTCGAGAGCTTTGATGTAATTCGCCAAGA 1253
DB 208 GAGTGTGAGAAGACCTCGCTTTGAACCTTTTGAGAGTTTGATGTAATTCATGCCCCAAG 149
QY 1254 GCTGATGCGGAGTTCTGTGCGCGCTTCTCTGAGGATGAGGATATGACCGGATGAA 1313
DB 148 GCCTGATGCGGAGTTTACGCGCTCCATTTCTCTGAGGATGAGGATATGAGAGACTAA 89
QY 1314 GCGGATAGGAGTGGACCAAGTATGCGGAGTACGTTGTTAG 1356
DB 88 GCGGATAGGAGTGGACCAAGTATGCGCAAGTATATTTGGGTAG 46

RESULT 11
BI191997 518 bp mRNA linear EST 10-JUL-2001
LOCUS BI191997
DEFINITION 14b10fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA

RESULT 12
B1187780/c
LOCUS B1187780 457 bp mRNA linear EST 10-JUL-2001
DEFINITION b2d04fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone b2d04fs 3', mRNA sequence.

ACCESSION B1187780.1 GI:14661459
VERSION EST.
KEYWORDS Fusarium sporotrichioides
SOURCE Fusarium sporotrichioides
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 457)
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Other ESTs: b2d04fs.r1
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Farrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 655 5e-70 gi|4378982|gb|AAD197 (AF127176)
 trichothecene3-O-acetyltransfer
 Seq primer: M13-20
 High quality sequence stop: 257.

FEATURES
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 /mol_type="mRNA"
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 /clone="b2d04fs"
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 /note="vector: pBluescript SK-; Site 1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript"

ORIGIN
 Query Match 19.8%; Score 268.4; DB 4; Length 457;
 Best Local Similarity 80.0%; Pred. No. 1.3e-67;
 Matches 328; Conservative 0; Mismatches 81; Indels 1; Gaps 1;
 QY 947 ACTGACCATCGCGAATGCCAACAGTCACTCGCGCAACAGCATCAGCCCTTCGTT 1006
 DB 454 ACTGACCGTGC CGGAATGCCAACGA-ACCTTTGGCGCAACAGCATCAGCCTCGCT 396
 QY 1007 CAGAACTCGACCCCGGAGCATGCGCCAGCAAGAGGTCTTCGCGAGTACTCTGCACA 1066
 DB 395 CGGAATCAACAGTGATCGTTTTCGCGAGCAACACAAGCTTTGGCGACGTACATGCATG 336
 QY 1067 ACAACCCGCAAGTCCAACTGATCCCTGACGCTGATGCGGACCCACTTACCAGCGTCA 1126
 DB 335 GCCTGCCTGACAAGTCGAGCGCTCTCCCTGACCGCGGATGCGAATCCGTCAACAGCATCA 276
 QY 1127 TGCTGAGTTCCTTGGCCAAAGTGGGAGTCTCGGGATTACGACTTTGGGCTCGGACTGGGTA 1186
 DB 275 TGCTGAGTTCCTTGGCCAAAGTGGGAGTCTCGGGAGTATGACTTTGGGTTTGGACTGGGTA 216
 QY 1187 AGCCCGAGACTGTGAGACGGCCAACTTTTGGACCTGTTTGAGAGCTTGATGTACTTATGTC 1246
 DB 215 AGCTTGAGAGTGTGAGAGAGACCTCGCTTTGAACCTTTTGAGAGTTTGAATGACTTATGTC 156

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QY 1247 CCAGAGCCTGATGCGGAGTTCTGTGGCGGCTTTCTCTGAGGATGAGGATATGGACC 1306
Db 155 CCAAGAAGCCTGATGCGGAGTTTACCGCGCTCCATTTCTCTGAGGATGAGGATATGGAGA 96
QY 1307 GATTGAAGCGGTAAGGAGTGACCAAGTATGCGCAGTACGTTGGTTAG 1356
Db 95 GACTAAAGCGGATGAGGATGGAACAAGTACGCAAAAGTATATTGGGTAG 46

RESULT 13
BI192452          392 bp  mRNA  linear  EST 10-JUL-2001
LOCUS m4b09fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION library Fusarium sporotrichioides cDNA clone m4b09fs 5', mRNA
sequence.
ACCESSION BI192452
VERSION BI192452.1 GI:14666131
KEYWORDS Fusarium sporotrichioides
SOURCE Fusarium sporotrichioides
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE 1 (bases 1 to 392)
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
Beremand,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Other ESTs: m4b09fs.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Is the best homolog from a blastx search of Genbank nr 04-09-01
557 3e-57 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: T3
High quality sequence stop: 361.
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1. .392
/organism="Fusarium sporotrichioides"
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cDNA library"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"

ORIGIN
Query Match 19.0%; Score 258; DB 4; Length 392;
Best Local Similarity 80.2%; Pred. No. 1.5e-64;
Matches 316; Conservative 0; Mismatches 75; Indels 3; Gaps 1;

QY 347 TCGCGCCAAAGGAGAGCTTACCTATTGGACCTGGTACTGTCGCCGACGCCAACGCTTG 406
Db 1 TCGCTCCGAGGAAGACATTAGCTATCGGACCTGGCAATGGCCCAACGACCCGAGCCTG 60

QY 407 TAATTTCTATGAGCTCACTTCATCAGGGCGGACTCATCTCACTGTCACGGACAGC 466
Db 61 TGTGTGTTATGCACTCACTTCATTAAAGGCGGACTCATCTCACTGTCACGGACAGC 120

QY 467 ACGGTGCTATGGATATGTTAGGCAAGATGCGGTGATCCGTCTACTCTCTCAAGCGCTGCC 526
Db 121 ATGGTGCTATGGACATGACAGGACAGATGCAATTATTGCTCTTCTCTCAAGCGCTGCC 180

QY 527 GTAAACGACCCATTACCGGAAGAGGAATGACGGCCCATGAACCTCGATCGCAAGACGATAG 586

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Db 181 GCAACGAATTATTCACCGAGGAGAAATCTCGCCATGAACCTCGATCGCAACCGTAG 240
QY 587 TTCTCTTACCTTGAAAATATACGATTTGGCCCGAGGTAGATCATCATGATTTGTCAAAGCTG 646
Db 241 TCCCTCTCTCTGAAAACATACAAAGTTGGTCTGAGCTATACCACCATGCGCCAAACC-- 298
QY 647 ATGTAGCTGCTGCTGACGCTGTTCTCACGCCGCTAGTCCAAGCTGGGCGTTCTTCACAT 706
Db 299 -TGGCGCTGCTGGCGACGCTCCACCGCACCGCCCAAGCAAGCTGGGCGTTCTTTTCAT 357
QY 707 TCAGCCCCCAAGCCATGTCAGAGCTCAAGATGC 740
Db 358 TCACTCCCAAGGCCCTCTCGGAGCTGAAAGAGCG 391

RESULT 14
BI192498/c          423 bp  mRNA  linear  EST 10-JUL-2001
LOCUS m4f10fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION library Fusarium sporotrichioides cDNA clone m4f10fs 3', mRNA
sequence.
ACCESSION BI192498
VERSION BI192498.1 GI:14666177
KEYWORDS Fusarium sporotrichioides
SOURCE Fusarium sporotrichioides
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE 1 (bases 1 to 423)
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
Beremand,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Other ESTs: m4f10fs.r1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Is the best homolog from a blastx search of Genbank nr 04-09-01
652 3e-68 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: M13-20
High quality sequence stop: 290.
Location/Qualifiers
1. .423
/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"
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cDNA library"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"

ORIGIN
Query Match 18.8%; Score 254.8; DB 4; Length 423;
Best Local Similarity 79.6%; Pred. No. 1.3e-63;
Matches 301; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 979 CTCGGCGCAACAGCATCACGCTTCTGTTCCAGAACTGACCCCGAGCATGGCCACGCA 1038
Db 423 CTTGGCGCAACAGCATCACGCTTCTGTTCCAGAACTGTTGCGTTCGTCAGACGCA 364
QY 1039 ACAAGAGTCTCGGAGCTACCTGTCACAAACCCCGCAAGTCCCAACGTTCCCTGAGC 1098

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Db      363 ACACAAGCTTTGGCGACGTACATGATGCGCTGCTGACACAGTCGAGCGTCTCCCTGACC 304
QY      1099 GCTGATGCCGACCCATCTACAGCGTCATGCTGAGTTCTTGGGCCAAGGTGGACTCTGG 1158
Db      303 GCGGATGCGGAATCCGTCAGAGAGCATCATGCTGAGTCTCTGGGCCAAGGTGGATGCTGG 244
QY      1159 GATTACGACTTTGGGCTCGGACTGGGTAAAGCCGAGACTGTGAGACGGCCAAATCTTTGAG 1218
Db      243 GAGTATGACTTTGGGTTTGGACTGGGTAAAGCTGAGAGTGTGAGAAGACCTCGCTTTGAC 184
QY      1219 CTGTTGAGAGCTGTGATGATCTTATGCCCAGAGACCTGATGGCGAGTCTGTGCGGGG 1278
Db      183 CTTTTTGAGAGTTTGTATGTACTTATGCCCAGAGACCTGATGGGAGGTTTACGGCGTCC 124
QY      1279 CTTTCTCTGAGGATGAGGATATGAGACGATTAAGCGGCGATTAAGGAGTGGACCAAGTAT 1338
Db      123 ATTCTCTGAGGATGAGGATATGAGAGACTAAAGCGGCGATGAGGAGTGGACAAAGTAC 64
QY      1339 GCGCAGTACGTTGGTTAG 1356
Db      63 GCAAAGTATATGGGTAG 46

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RESULT 15

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BI201353 490 bp mRNA linear EST 10-JUL-2001
LOCUS p2e12fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION library Fusarium sporotrichioides cDNA clone p2e12fs 5', mRNA
sequence.

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ACCESSION BI201353
VERSION BI201353.1 GI:14667325
KEYWORDS EST.
SOURCE Fusarium sporotrichioides

```

ORGANISM

```

Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

```

REFERENCE

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1 (bases 1 to 490)

```

```

AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
Beremand,M. and Roe,B.

```

TITLE

```

Analysis of a Fusarium sporotrichioides EST database

```

JOURNAL

```

Unpublished (2001)

```

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Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

```

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Department of Chemistry and Biochemistry

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Advanced Center for Genome Technology, University of Oklahoma

```

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620 Parrington Oval, Norman, OK 73019, USA

```

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Tel: 405 325 4912

```

```

Fax: 405 325 7762

```

```

Email: broe@ou.edu

```

```

Contact Dr. Marian Beremand regarding clone availability Included

```

```

is the best homolog from a blastx search of Genbank nr 04-09-01

```

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656 1e-68 gi|4378882|gb|AAD197 (AF127176)

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trichothecene3-O-acetyltransfer

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Seq primer: T3

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High quality sequence stop: 443.

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FEATURES

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Location/Qualifiers
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/mol_type="mRNA"
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/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"

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ORIGIN

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Query Match 18.5%; Score 251.2; DB 4; Length 490;
Best Local Similarity 81.1%; Pred. No. 1.6e-62;
Matches 292; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

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QY      3 GGCTTTCAAGATACAGTCTCGACACCCCTCGGCGAGTACCAGGCCTCCTTTTCGATCTACAC 62
Db      129 GTCTTTTGACATAGAGCTCGACATCATCGGCCAGCAACCGCTCTCTTTTCAATCTACAC 188
QY      63 CCAATCAGTCTCTCTACCCCGTCTCTGATTCTCTCAATATCCACTATTGTGAGCAGAC 122
Db      189 CCAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCAGTATCCACCATCGTCAGCAGAC 248
QY      123 CTTGAGCAAGGTCTTAAAGCGCTTCTCCGAAAGCCGTCCTCCATGGGTGCGAGCCAGGTCAA 182
Db      249 CTTGAGGAAGGCCTTAAACCGCTCTCTCAAACTTCCATGGGTGCGGGCCAGGTCAA 308
QY      183 AGCCGAGGGCAATTAGCGAGGGGAAACACAGGAACTTCTCTTTATCGTCCCTTTTGAGGAGCT 242
Db      309 GACCGAGGGCATCAGCGAAGGAAACACAGGAACTTCCAAGATCATTCATATGAGGAGAC 368
QY      243 TCCTCGTCTGTGATGAAAGACCTCCGCGATGATCCTTTCAGCGCCAGCATCGAGGGTAT 302
Db      369 ACCCGCTCTTGTGGTGAAGACCTCCGATGATGATTCCTCAGGGCCAAAGTCGAGGGGTT 428
QY      303 GAGAAAGCGGGATACCCCTATGGCGATGTTTTCAGGAGAAACATCATTCGCGCCAAAGAAAGAC 362
Db      429 GAGAAAGCGGGTTTCCCTTAGAGATGTTTTCAGGAGAAACGTCGTCGCTCCGAGGAAGAC 488

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Search completed: January 23, 2005, 17:48:20

Job time : 4738 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 21:19:40 ; Search time 731 Seconds
(without alignments)
9737.640 Million cell updates/sec

Title: US-10-614-954-5
Perfect score: 1356
Sequence: 1 atggtttcaagatacagct.....atgcgcagtaoatgttgtag 1356

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1356	100.0	1356	3	AA54209 Sequence
2	1356	100.0	1356	12	ADN37285
3	1340	98.8	1605	3	Aaz89368 F. Gramin
4	915.6	67.5	1403	3	AA54206 Sequence
5	915.6	67.5	12949	3	AA54213 Transform
6	915.6	67.5	13737	3	AA54212 Transform
7	249.8	18.4	1425	3	AA54210 Sequence
8	146.2	10.8	695	3	AAFI2071 Aspergill
9	116.2	8.6	482	8	ABZ54817 Aspergill
10	50.4	3.7	2000	8	ADA71938 Rice gene
11	40.2	3.0	2000	8	ADA71938 Rice gene
12	39.8	2.9	663	12	AD181367 M. tuberc
13	39.8	2.9	110000	4	AA199682_42
14	39.8	2.9	110000	4	AA199683_42
15	36.4	2.7	1605	2	AAT37310 Aromatic
16	35.8	2.6	2463	10	ADB68880
17	35.6	2.6	1459	6	ABQ33693 Oligonuel
18	35.6	2.6	1459	6	ABQ33692 Oligonuel
19	35.6	2.6	1463	6	ABQ14443 Oligonuel
20	35.6	2.6	1463	6	ABQ14442 Oligonuel
21	35.6	2.6	110000	12	ADN46845_12
					Continuation (13 o

C	22	35.6	2.6	110000	12	ADN47591_08	Continuation (9 of
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C	26	35.6	2.6	110000	12	ADN47960_08	Continuation (9 of
C	27	35.4	2.6	4526	10	ADB52532_08	Abd52532 Primary r
						AAH41223 Pyrococcu	
						Adf44504 Mouse kin	
						Adf44505 Mouse kin	
						Adf44491 Mouse kin	
						Adi42469 Plant tra	
						Adi42469 P. aerugi	
						Adi181791 P. aerugi	
						Adi181732 P. aerugi	
						Abd17428 Pseudomon	
						Abd17540 Pseudomon	
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						Abd17540 N. gonorr	
						Abd17540 Prokaryot	
						Abd17540 DNA encod	
						Abd17540 Oligonuel	
						Abd17540 Oligonuel	
						Abd17540 Oligonuel	
						Abd17540 Genomic f	

ALIGNMENTS

RESULT 1
AA54209
ID AAA54209 standard; DNA; 1356 BP.
XX
AC AAA54209;
DT 15-SEP-2003 (revised)
DT 26-FEB-2001 (first entry)
XX
DE Sequence encoding trichothecene resistance polypeptide.
XX
KW Trichothecene resistance; resistant; crop protection; mycotoxin; fungus;
KW wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;
KW ds.
XX
OS Gibberella zeae.
XX
FH Key Location/Qualifiers
FT CDS 1..1356
FT /tag= a
FT /product= "Trichothecene resistance polypeptide"

XX WO200060061-A2.
XX PD 12-OCT-2000.
XX PF 29-MAR-2000; 2000WO-EP002769.
XX PR 31-MAR-1999; 99US-00282995.
XX PR 11-FEB-2000; 2000US-00502852.
XX PA (NOVS) NOVARTIS AG.
XX PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX PI Hohn TM, Peters C, Salmerton JM, Read JN, Dawson JL;
XX DR WPI; 2000-679374/66.
XX DR P-PSDB; AAB03935.
XX PT plant cell for preventing mycotoxin contamination of wheat, maize, barley
XX PT or rice plant, comprises heterologous polynucleotide encoding gene
XX PT product expressed in cell, having trichothecene resistance activity.
XX PS Claim 8; Page 48-49; 62pp; English.

XX A heterologous gene encoding a gene product which confers trichothecene
 CC resistance can be used to transform plant cells to make them resistant to
 CC fungal infection. The transformation method is useful for preventing
 CC mycotoxin contamination of a plant, particularly a crop plant such as
 CC wheat, maize, barley or rice, and for reducing and/or preventing the
 CC growth of a fungus of the genus *Fusarium* that produces a trichothecene,
 CC preferably comprising a C-3 hydroxyl group, by growing transformed crop
 CC plants in an area which is moderate to severe fungal infestation.
 CC (Updated on 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 1356 BP; 319 A; 385 C; 349 G; 303 T; 0 U; 0 Other;

Query Match 100.0%; Score 1356; DB 3; Length 1356;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTTTCAAGATACAGCTCGACACCCCTCGGCAGCTACCGAGGCTCTCTTCGATCTAC 60
 DB 1 ATGGCTTTCAAGATACAGCTCGACACCCCTCGGCAGCTACCGAGGCTCTCTTCGATCTAC 60
 QY 61 ACCCAATCAGTCTCTTACCCGCTCTGATCTCTCAATATCCCACTATTCTCAGC 120
 DB 61 ACCCAATCAGTCTCTTACCCGCTCTGATCTCTCAATATCCCACTATTCTCAGC 120
 QY 121 ACCTTCGAGCAAGGTCTTAAGCGCTTCTCGAAGCGCTCCCATGGGTCCGAGCCAGGTC 180
 DB 121 ACCTTCGAGCAAGGTCTTAAGCGCTTCTCGAAGCGCTCCCATGGGTCCGAGCCAGGTC 180
 QY 181 AAAGCCGAGGCGATTAGCGAGGGAACAACAGGAATCTCTTTATCGTCCCTTTTGAAGAC 240
 DB 181 AAAGCCGAGGCGATTAGCGAGGGAACAACAGGAATCTCTTTATCGTCCCTTTTGAAGAC 240
 QY 241 GTTCTCTGTTTGTAGTGAAGACCTCCGCGATGATCTTCAGCGCCACGATCGAGGCT 300
 DB 241 GTTCTCTGTTTGTAGTGAAGACCTCCGCGATGATCTTCAGCGCCACGATCGAGGCT 300
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 QY 361 ACCTTACCTATTGGACTGGTACTGGTCCGAGCAGCCAAAGCTGTATTTCTATTGCGAG 420
 DB 361 ACCTTACCTATTGGACTGGTACTGGTCCGAGCAGCCAAAGCTGTATTTCTATTGCGAG 420
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 DB 481 ATGTAGGCCAAGATGCGGTGATCCGCTACTCTTCCAAAGCGGTGCGGTAAACGCCATTTC 540
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 QY 721 ATGTACAGCTCAGGATGCTGTACCAAGACTCTTCAGCAGATCAACAAAGTTCTGTGTCG 780
 DB 721 ATGTACAGCTCAGGATGCTGTACCAAGACTCTTCAGCAGATCAACAAAGTTCTGTGTCG 780
 QY 781 ACTGACGATGCTCTTTGGCGGCTTCTATCTGGAATTCGGCTCTCGCGTGGCTCTCGAAGA 840
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QY 841 ATCGATCGCTCTGCACCTACCGAGTTCTGCGGTGCTGTTGATGCTCGACCGCAATGGGT 900
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 QY 901 GTCTCGAACAATACCCAGAGCTTCTTCAAAACATGACCTTACCAACTCGACCATCGGC 960
 DB 901 GTCTCGAACAATACCCAGAGCTTCTTCAAAACATGACCTTACCAACTCGACCATCGGC 960
 QY 961 GAAATCGCAACAGAGTCACTCGGCGCAACAGCATCACGCCCTTGGTTCAGAACTCGACCCC 1020
 DB 961 GAAATCGCAACAGAGTCACTCGGCGCAACAGCATCACGCCCTTGGTTCAGAACTCGACCCC 1020
 QY 1021 GCGAGCATGCGCCAGAGGAAACAGAGGTCTCGCGAGCTACCTGCAACAACCCCGACAAG 1080
 DB 1021 GCGAGCATGCGCCAGAGGAAACAGAGGTCTCGCGAGCTACCTGCAACAACCCCGACAAG 1080
 QY 1081 TCCAACTGATCCCTGAGCGCTGATGCGGAGCCCATCTACGAGCTCATGCTGAGTCTTTGG 1140
 DB 1081 TCCAACTGATCCCTGAGCGCTGATGCGGAGCCCATCTACGAGCTCATGCTGAGTCTTTGG 1140
 QY 1141 GCCAAGGTGGGACTCTGGGATTCAGACTTTGGGCTCGGACTGGGTAAGCCGAGACTGTG 1200
 DB 1141 GCCAAGGTGGGACTCTGGGATTCAGACTTTGGGCTCGGACTGGGTAAGCCGAGACTGTG 1200
 QY 1201 AGACGGCCAACTTTGAGCCCTGTTGAGAGCTTGTATGCTTATGCCCCAAGAACCTTGAT 1260
 DB 1201 AGACGGCCAACTTTGAGCCCTGTTGAGAGCTTGTATGCTTATGCCCCAAGAACCTTGAT 1260
 QY 1261 GCGAGTTCTGCGGGCGCTTTCTCTGAGGATGAGGATATGACCGATTGAAGGCGGAT 1320
 DB 1261 GCGAGTTCTGCGGGCGCTTTCTCTGAGGATGAGGATATGACCGATTGAAGGCGGAT 1320
 QY 1321 AAGGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG 1356
 DB 1321 AAGGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG 1356

RESULT 2
 ADN37285
 ID ADN37285 standard; DNA; 1356 BP.
 XX
 AC ADN37285;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Trichothecene 3-O-acetyltransferase encoding DNA SEQ ID NO:29.
 XX
 KW maternal tissue; plant seed; plant;
 KW bifunctional alpha-amylase subtilisin inhibitor gene promoter;
 KW alpha-amylase inhibitor promoter; ASI promoter; plant protectant;
 KW virucide; vaccine; resistance; infection; *Fusarium graminearum*;
 KW trichothecene 3-O-acetyltransferase; enzyme; gene; ds.
 XX
 OS Gibberella zeae.
 XX
 FH Key Location/Qualifiers
 CDS 1..1356
 FT /*tag= a
 FT /product= "Trichothecene 3-O-acetyltransferase protein"
 PN WO2004035790-A1.
 XX
 PD 29-APR-2004.
 XX
 PF 17-OCT-2003; 2003WO-AU001381.
 XX
 PR 17-OCT-2002; 2002AU-00952143.
 XX
 PA (MOLE-) MOLECULAR PLANT BREEDING NOMINEES LTD.
 PA (GRAI-) GRAINS RES & DEV CORP.
 XX
 PI Furtado A, Henry RJ;
 XX

Wed Jan 26 11:53:55 2005

AAZ89368;
15-SEP-2003 (revised)
09-JUN-2000 (first entry)
F. graminearum trichothecene 3-O-acetyltransferase DNA.
Trichothecene 3-O-acetyltransferase; selective marker; ds.
Gibberella zeae.
Key Location/Qualifiers
CDS 135..1490
/*tag= a
/product= "trichothecin 3-O-acetyltransferase"
JP2000032985-A.
02-FEB-2000.
15-JUL-1998; 98JP-00200280.
15-JUL-1998; 98JP-00200280.
(RIKA) RIKAGAKU KENKYUSHO.
(YAMA/) YAMAGUCHI I.
WPI; 2000-274037/24.
P-PSDB; AAY51848.
Trichothecin 3-O-acetyltransferase gene useful as a selective marker in
gene manipulations in eukaryotic host cells.
Claim 3; Page 16-18; 25pp; Japanese.
This invention describes a novel protein with trichothecin 3-O-
acetyltransferase activity. The gene is used as a selective marker in a
gene manipulation using eukaryote as the host cell. This sequence encodes
the trichothecin 3-O-acetyltransferase isolated from Fusarium
graminearum. (Updated on 15-SEP-2003 to standardise OS field)
SQ Sequence 1605 BP; 397 A; 459 C; 393 G; 356 T; 0 U; 0 Other;
Query Match 98.8%; Score 1340; DB 3; Length 1605;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
1 ATGGCTTTCAAGATACAGCTCGACACCTCGGCCAGCTACAGGCTCTCTTCGATCTAC 60
135 ATGGCTTTCAAGATACAGCTCGACACCTCGGCCAGCTACAGGCTCTCTTCGATCTAC 194
61 ACCCAATCAGTCTCTTACCCGCTCTCTGATTCCTCTCAATATCCACTATTGTTCAGC 120
195 ACCCAATCAGTCTCTTACCCGCTCTCTGATTCCTCTCAATATCCACTATTGTTCAGC 254
121 ACCTTCGAGCAAGGTCTTAAAGCGTCTTCCGAAGCGCTCCCATGGGTCGAGGCCAGGTC 180
255 ACCTTCGAGCAAGGTCTTAAAGCGTCTTCCGAAGCGCTCCCATGGGTCGAGGCCAGGTC 314
181 AAAGCCGAGGCGATTAGCGAGGGAACACAGGAACCTTCCTTTATCGTCCCTTTTGAGGAC 240
315 AAAGCCGAGGCGATTAGCGAGGGAACACAGGAACCTTCCTTTATCGTCCCTTTTGAGGAC 374
241 GTTCTCTGTTGTAGTCAAGAGCTCGCGATGATCTTCAGCGCCACGATCGAGGGT 300
375 GTTCTCTGTTGTAGTCAAGAGCTCGCGATGATCTTCAGCGCCACGATCGAGGGT 434
301 ATGAGAAAGGGGGATACCTATGCGGATGTTTGAAGGAACATCATCGCGCCCAAGGAAG 360
435 ATGAGAAAGGGGGATACCTATGCGGATGTTTGAAGGAACATCATCGCGCCCAAGGAAG 494
361 ACGTTACCTATTGGACCTGGTACTGTCGCGACCCCAAGCGCTGTAATTTCTATTGCGAG 420

495 ACGTTACCTATTGGACCTGGTACTGCGCCCGCAGCAACCAAGCCTGTGATTTCTATTGCGAG 554
421 CTCAACTTTCATCAAGGGCGGACTCATCTCCTCAACGAGCAGCAGCGTGTATGGAT 480
555 CTCAACTTTCATCAAGGGCGGACTCATCTCCTCAACGAGCAGCAGCGTGTATGGAT 614
481 ATGGTAGGCCAAGATGCGGTGATCCGCTCTACTCTCAAGGCGTGCCTTAACGCCATTTC 540
615 ATGGTAGGCCAAGATGCGGTGATCCGCTCTACTCTCAAGGCGTGCCTTAACGCCATTTC 674
541 ACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGAGATGTTCTTACCTTTGAA 600
675 ACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGAGATGTTCTTACCTTTGAA 734
601 AACTATACGATTGCGCCCGGAGTAGATCATCAGATTGTCAAAGCTGATGTAGTGTGGT 660
735 AACTACACGATTGGCCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGTGTGGT 794
661 GACGCTGTTCTCACGCCGGTCAGTGCAAGTGGGGCTTCTTCACTTACGCCCCAAGGCC 720
795 GACGCTGTTCTCACGCCGGTCAGTGCAAGTGGGGCTTCTTCACTTACGCCCCAAGGCC 854
721 ATGTACAGCTCAAGATGCTGTACCAAGCTTTCAGCATCAACAAAGTTTGGTGTGG 780
855 ATGTACAGCTCAAGATGCTGTACCAAGCTTTCAGCATCAACAAAGTTTGGTGTGG 914
781 ACTGACGATGCTCTTTGCGGCTTTCATCTGGAATTCGGCTCTCGCGTGGCTCGCAAGA 840
915 ACTGACGATGCTCTTTGCGGCTTTCATCTGGAATTCGGCTCTCGCGTGGCTCGCAAGA 974
841 ATCGATGGCTTGCACTTACCGAGTTCGCGTCTGTTGATGCTGACCGGCAATGGT 900
975 ATCGATGGCTTGCACTTACCGAGTTCGCGTCTGTTGATGCTGACCGGCAATGGT 1034
901 GTCTCGAACAATACCCAGGCTTCTTCAAAACATGACCTACCAACAATCGACCATCGGC 960
1035 GTCTCGAACAATACCCAGGCTTCTTCAAAACATGACCTACCAACAATCGACCATCGGC 1094
961 GAAATCGCAACAGAGTCACTCGGCGCAACAGCATCAAGCTTCTGATGAGTCTGAGTCT 1020
1095 GAAATCGCAACAGAGTCACTCGGCGCAACAGCATCAAGCTTCTGATGAGTCTGAGTCT 1154
1021 GCGACATGCGCCGCAAGAGGCTCTCGGAGTACCTGCGACCAACAACCCGCAAG 1080
1155 GCGACATGCGCCGCAAGAGGCTCTCGGAGTACCTGCGACCAACAACCCGCAAG 1214
1081 TCCAAAGTATCCCTGACGCGTGTATGCGGACCCATCTACCGGCTCATGCTGAGTCTTGG 1140
1215 TCCAAAGTATCCCTGACGCGTGTATGCGGACCCATCTACCGGCTCATGCTGAGTCTTGG 1274
1141 GCGAAGTGGGACTCTCGGATTAACGCTTTGGGCTCGGACTGGGTAAAGCCGAGACTGTG 1200
1275 GCGAAGTGGGACTCTCGGATTAACGCTTTGGGCTCGGACTGGGTAAAGCCGAGACTGTG 1334
1201 AGACGCGCAATCTTTGAGCTGTTGAGAGCTTGTATGATCTTTATGCCCAAGAGCTGAT 1260
1335 AGACGCGCAATCTTTGAGCTGTTGAGAGCTTGTATGATCTTTATGCCCAAGAGCTGAT 1394
1261 GCGGAGTCTGTGCGCGCTTTCTGTAGGGATGAGGATATGAGCCGATTGAGCGGGAT 1320
1395 GCGGAGTCTGTGCGCGCTTTCTGTAGGGATGAGGATATGAGCCGATTGAGCGGGAT 1454
1321 AAGGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG 1356
1455 AAGGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG 1490

RESULT 4
AA54206
ID AAA54206 standard; cdna; 1403 BP.
XX
AC
AA54206;
XX

Wed Jan 26 11:53:55 2005

RESULT 5	243	TCCTCGTGTGTAGTGAAGACCTCGCGATGATCTTTCAGCGCCCAACGATCGAGGTAT	302
AAA54213	11521	ACCCGTCCTTGTGTGAAGACCTTCGTGATGATCTTCAGCGCCCAACGATCGAGGGTT	11580
XX	AC	AAA54213;	
XX	DT	26-FEB-2001 (first entry)	
XX	XX	Transformation vector pNOV1704.	
DE	XX	Tricothecene resistance; resistant; crop protection; mycotoxin; fungus;	
XX	XX	wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;	
KW	XX	ds.	
XX	OS	Synthetic.	
XX	PN	WO200060061-A2.	
XX	PD	12-OCT-2000.	
XX	XX	29-MAR-2000; 2000WO-EP002769.	
XX	XX	31-MAR-1999; 99US-00282995.	
PR	XX	11-FEB-2000; 2000US-00502852.	
XX	PA	(NOVS) NOVARTIS AG.	
XX	PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.	
XX	PI	Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;	
XX	XX	WPI; 2000-679374/66.	
XX	PT	Plant cell for preventing mycotoxin contamination of wheat, maize, barley	
PT	PT	or rice plant, comprises heterologous polynucleotide encoding gene	
PT	PT	product expressed in cell, having tricothecene resistance activity.	
XX	BS	Disclosure; Page 58-62; 62pp; English.	
XX	CC	A heterologous gene encoding a gene product which confers tricothecene	
CC	CC	resistance can be used to transform plant cells to make them resistant to	
CC	CC	fungal infection. The transformation method is useful for preventing	
CC	CC	mycotoxin contamination of a plant, particularly a crop plant such as	
CC	CC	wheat, maize, barley or rice, and for reducing and/or preventing the	
CC	CC	growth of a fungus of the genus Fusarium that produces a tricothecene,	
CC	CC	preferably comprising a C-3 hydroxyl group, by growing transformed crop	
CC	CC	plants in an area which is moderate to severe fungal infestation. Plasmid	
CC	CC	pNOV1704 comprises the Zea mays ubiquitin promoter, the phosphate mannose	
CC	CC	isomerase selectable marker and the nopaline synthase termination	
CC	CC	sequence. pNOV1704 further comprises the Zea mays ubiquitin promoter	
CC	CC	operably linked to the tricothecene 3-O-acetyl transferase sequence	
CC	CC	given in GENESEQ record AAA54206 and the nos termination sequence	
XX	XX	Sequence 12949 BP; 3194 A; 3146 G; 3143 G; 3466 T; 0 U; 0 Other;	
SQ	Query Match	67.5%; Score 915.6; DB 3; Length 12949;	
	Best Local Similarity	80.3%; Pred. No. 3.7e-278;	
	Matches 1087; Conservative	0; Mismatches 264; Indels 3; Gaps 1;	
QY	3	GGCTTTCAAGATACAGCTCGACACCTCGGCAGCTACCGAGCTCCTTTTCGATCTACAC	62
Db	11281	GTCTTTTGACATAGAGCTCGACATCATCGGCACCAACCGGCTCTCTTTCAATCTACAC	11340
QY	63	CCAATAGTCTCTCTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTCAGCAC	122
Db	11341	COAGATCAGTCTCGTTTACCCCGTCTCTGATTCCTCCAGTATCCCACTCGTCAGCAC	11400
QY	123	CTTCGAGCAAGTCTTAAGCGCTTCTCGAAGCGCTGCCATGGTTCGACCGCAGGTCAA	182
Db	11401	CCTTGAGGAAGCGCTTAAACCGCTCTCTCAAACCTTCCCATGGTTCGGGCCAGGTCAA	11460
QY	183	AGCCGAGGCGATTAGCGAGGAACACAGGAACCTTCCTTTATCGTCCCTTTTGAAGACGT	242
Db	11461	GACCCGAGGCGATCAGCGAAGGAACACAGGAACCTTCAGATCATTCATATGAGGAGAC	11520

QY	1323	GGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG	1356	Db	170	CCTTGAGGAGGCCTAAAGCGCCTCTCTCAAAACCTTTCCCATGGTTCGGGCGCGGCGCAGGTCAA	229
Db	12598	GGAGTGGACCAAGTACGCAAGTATATTGGGTAG	12631	QY	183	AGCCGAGGGCATTAGCGAGGAAACACACAGAACTTCCTTTATCGTCCCTTTTGGAGACGT	242
RESULT 6							
AA54212							
ID	AAA54212 standard; DNA; 13737 BP.						
AC	AAA54212;						
DT	26-FEB-2001 (first entry)						
XX	Transformation vector pAgroTRir.						
DE							
XX	Tricothecene resistance; resistant; crop protection; mycotoxin; fungus;						
KW	wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;						
KW	ds.						
OS	Synthetic.						
XX	WO200606061-A2.						
PN	12-OCT-2000.						
XX							
PF	29-MAR-2000; 2000WO-EP002769.						
XX							
XX	31-MAR-1999; 99US-00282995.						
PR	11-FEB-2000; 2000US-00502852.						
XX							
PA	(NOVS) NOVARTIS AG.						
PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.						
PI	Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;						
XX	WPI; 2000-679374/66.						
DR							
XX	Plant cell for preventing mycotoxin contamination of wheat, maize, barley						
PT	or rice plant, comprises heterologous polynucleotide encoding gene						
PT	product expressed in cell, having tricothecene resistance activity.						
XX	Disclosure; Page 54-58; 62pp; English.						
PS							
XX	A heterologous gene encoding a gene product which confers tricothecene						
CC	resistance can be used to transform plant cells to make them resistant to						
CC	fungal infection. The transformation method is useful for preventing						
CC	mycotoxin contamination of a plant, particularly a crop plant such as						
CC	wheat, maize, barley or rice, and for reducing and/or preventing the						
CC	growth of a fungus of the genus Fusarium that produces a tricothecene,						
CC	preferably comprising a C-3 hydroxyl group, by growing transformed crop						
CC	plants in an area which is moderate to severe fungal infestation. Plasmid						
CC	pAgroTRir comprises a selectable marker operably linked to a promoter and						
CC	terminator sequence and the tricothecene resistance gene described in						
CC	GENESEQ record AA54206 behind and in frame with the Arabidopsis thaliana						
CC	UBI 3 promoter and in front of and in frame with the nos polyadenylation						
CC	signal						
XX	Sequence 13737 BP; 3341 A; 3442 C; 3629 G; 3325 T; 0 U; 0 Other;						
SQ							
Query Match				67.5%; Score 915.6; DB 3; Length 13737;			
Best Local Similarity				80.3%; Pred. No. 3.8e-278;			
Matches 1087; Conservative				0; Mismatches 264; Indels 3; Gaps 1;			
QY	3	GGCTTTCAAGATACAGCTCGACACCTCGGCGAGCTTACCAGGCTCTCTTCGATCTACAC	62	Db	1083	CAACGTATCCCTGACGGGTGATGCGGACCCCATCTACACAGCGTCATGCTGAGTTCTTGGGC	1142
Db	50	GTCTTTTGACATGAGCTCGACATCATTCGCGCAGACACCGCTCTCTCTTCATCTACAC	109	QY	1127	GAGCGTCTCCCTGACCGCGGATGCGAATCCGTCAGCAGCATCATGCTGAGTTCCTGGGC	1186
QY	63	CCAAATCAGTCTCTCTACCCCGTCTCTGATTCTCTCAATATCCCACTATTGTGAGCAC	122	Db	1187	CAAGTGGGATGCTGGGAGTATGACTTTGGGTTTGGACTGGGTAAGCCCTGAGAGTGTGAG	1246
Db	110	CCAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCAGTATCCACCATGTCAGCAC	169	QY	1203	AGGCCAATCTTTGAGCGCTGTGAGAGCTTGATGACTTTATGCCCAAGACCTGTATGG	1262
QY	123	CTTCGAGCAAGGTCTTAAGCGCTTCTCCGAGCGCTCCCATGGTGGCGAGGCCAGGTCAA	182	Db	1247	AAGACCTCGCTTTGAACCTTTTGGAGAGTTGATGACTTTATGCCCAAGACCTGTATGG	1306

QY 1263 CGAGTCTCTGCGCGCTTCTCTGAGGATGAGATGAGCCGATGGAAGCGGATAA 1322
 Db 1307 GGAGTTTACCGGCTCCATTTCTCTGAGGATGAGATGAGAGACTAAAGCGGATGA 1366

QY 1323 GGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG 1356
 Db 1367 GGAGTGGACAAAGTACGCAAGTATATGGGTAG 1400

RESULT 7
 AAA54210
 ID AAA54210 standard; DNA; 1425 BP.
 XX AC AAA54210;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE Sequence encoding trichothecene resistance polypeptide.
 XX
 DE Trichothecene resistance; resistant; crop protection; mycotoxin; fungus;
 KW wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;
 KW ds.
 XX
 OS Saccharomycetes cerevisiae.
 XX
 FH Location/Qualifiers
 FT 1. .1425
 FT /*tag= a
 FT /product= "Trichothecene resistance polypeptide"
 XX
 XX W0200060061-A2.
 XX
 PD 12-OCT-2000.
 XX
 XX 29-MAR-2000; 2000WO-EP002769.
 XX
 XX 31-MAR-1999; 99US-00282995.
 PR 11-FEB-2000; 2000US-00502852.
 XX
 XX (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERM GES MBH.
 XX
 XX Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;
 PI
 XX
 DR WPI; 2000-679374/66.
 DR P-PSDB; AAB03936.
 XX
 XX Plant cell for preventing mycotoxin contamination of wheat, maize, barley
 PT or rice plant, comprises heterologous polynucleotide encoding gene
 PT product expressed in cell, having trichothecene resistance activity.
 XX
 XX Claim 8; Page 50-51; 62pp; English.
 PS
 XX A heterologous gene encoding a gene product which confers trichothecene
 CC resistance can be used to transform plant cells to make them resistant to
 CC fungal infection. The transformation method is useful for preventing
 CC mycotoxin contamination of a plant, particularly a crop plant such as
 CC wheat, maize, barley or rice, and for reducing and/or preventing the
 CC growth of a fungus of the genus Fusarium that produces a trichothecene,
 CC preferably comprising a C-3 hydroxyl group, by growing transformed crop
 CC plants in an area which is moderate to severe fungal infestation
 XX
 XX Sequence 1425 BP; 431 A; 305 C; 293 G; 396 T; 0 U; 0 Other;
 SQ

Query Match 18.4%; Score 249.8; DB 3; Length 1425;
 Best Local Similarity 51.9%; Pred. No. 7.7e-68;
 Matches 700; Conservative 0; Mismatches 622; Indels 27; Gaps 5;
 QY 16 CAGTCCGACCCCTCGGCGCAGCTACCGGCTCCTCTTCGATCTACACCCAAATCAGTCTC 75
 Db 64 CAACTTGATATTTGGGACACACACCTTCGCTATACAACTATACATCAATATGCTCT 123

QY 76 CTCTACCCCGCTCTCTGANTCCTCTCAATATCCCACTATTGTCAGCACCTTCGAGCAGGT 135
 Db 124 ATCTACCGTGTACAGATCCTTCTGCTCATGACCATTATCGTAATACCTTAACAAGAGGA 183
 QY 136 CTTAAGCGCTTCTCCGAAGCGTCCCATGGTGCAGGCCAGGTCAAAGCGGAGGCATT 195
 Db 184 CTTGAACAATTTGGCTAAATAATTTCCAGTGGCTAGCAGAAATGTCGTAATGAAGTGTCT 243
 QY 196 AGCGAGGGAACACAGGAACCTTCCTTTATCGTCTCCCTTTTGAGGACGTTCTCTGTTGTA 255
 Db 244 GACGAAGGTAACTGTGTACAGAAATTTGCCGTGAGCAAAATTCACAC---TTATC 300
 QY 256 GTGAAAGACCTCCCGATGATCTTTCAGCGCCACGATCGAGGTATGAGAAAGCGGGA 315
 Db 301 GTCCAAGATCTTCGAGAAGATCTGCTGCCCCCAACAATGGATTTCGCTTGAAGAGCTGAC 360
 QY 316 TACCTATGGCGATGTTTGAAGAAACATCATCCGCGCAAGGAAGAGCTT-----ACCT 369
 Db 361 TTCTTATCTACATGTATAGCAAAAGACTTTTGGCTTGCATGACTATCAATCCACCT 420
 QY 370 ATTGACCTGTACTGTGTCGCGACGCCCAAGCCTGTAAATTTATTGACGCTCAACTTC 429
 Db 421 GGAAACACTATAGGTATGGCGCCCAAGAGTGGGCTGTATTGTCAGTTCAAGCAAACTTT 480
 QY 430 ATCAAGGCGGACTCATCTCCTCACTGTCAAAGGAGTGGCTTACGACCCATTCACCGAAGAG 549
 Db 481 ATCTCGGCGGCTCGTCTTAACTATTGTTCGGGAGCACAATATATTGGATATACAGGA 540
 QY 490 CAAGATGGGTGATCCGCTACTCTCCAAGCGTGGCGGTACGACCCATTCACCGAAGAG 549
 Db 541 CAGGAAAGTATCACTCACTTGTCTCAATAAATCTTGGCCACCAAAACCTTCTCTGATGA 600
 QY 550 GAAATGACGGCCATGAACCTCGATGCGAAGACGATGTTCTTACCTTGAATAAATATACG 609
 Db 601 GAACCTGCTCATTTGGAAATATAGATAAAGCAAACTATTCTCTTTGTTGATGAACCTTTG 660
 QY 610 ATT----GGCCCCGAGTAGATCATCAGATTCTCAAGCTGATGATGCTGGTGGTACGCT 666
 Db 661 GAAACCGACACACGCTAGTTTCATGAATAATAGTGGAAACCTCTAGNAATACAGTGGAG 720
 QY 667 GTTCTCAGCGCGTCACT-----GCAAGCTGGGCGTTCTTCAATTCAGCCCCAAG 717
 Db 721 GAAAGGAACAGCTTTGTTCTTCGAACCTACTTGGGCTTATGTAATTTCTGCTATC 780
 QY 718 GCATGTACAGCTCAAGATGCTGTACCAAGACTCTTGAGCGCATCAACAAGTTCGTG 777
 Db 781 TCATTGCAGAAATCTGAGGATTTTGGCAATGCAGACATGATCTTCTGGCACAAAATTTGTC 840
 QY 778 TCGACTGACGATGCTCTTTTGGCGTTTCATCTGGAATCGGCTCTCGGCTGCGTCTCGAA 837
 Db 841 TCCACTGATGATATCGTCACTGCTTTCACTGGAATCAGTTTCTCGAGCCGTTTATCT 900
 QY 838 AGAATCGATGGCTCTGCACCTACCGAGTTCTGCCGCTGCTGTTGATGCTCGACCGGCAATG 897
 Db 901 CGACTTAAACAGAAACGAAATCAAATTTAGGGCGTGTGTGATGTTAGAAAACGGCTA 960
 QY 898 GGTGTCTGAACAACACTACCGAGCCCTTCTTCAAAACATGACCTTACCAACTCGACCATC 957
 Db 961 GGACTCCCCGAAACGTTATTCAGGGTTATTAGTCAACATGACCTTTAAATACAGTTCCCTG 1020
 QY 958 GCGGAAATCGCAACGAGTCACTCCGCGCAACAGCATCACGCTTCTGTTTCAAGACTCGAC 1017
 Db 1021 AAAGCTTGATCATAAAGTTTGGCGCTTCTTGCATCACAGATTCGAGGAAGCTAGAC 1080
 QY 1018 CCGCGGAGCA-----TGCGCCAGCGAAACAGAGTCTCGCGACGTCTCGCACACACAC 1071
 Db 1081 CTTAAAGTCTTCGATTTGGCTTATAATCATGCGCACTTGTACGCTCTCTTAGCCGATGC 1140
 QY 1072 CCGGACAAGTCAACGATATCCCTGAGCGGTGATGGGACCCATCTACAGCGCTCATGCTG 1131
 Db 1141 CCGGACAAAGCAAGGTTTCTATACCTCAACCAATGATCTTATCTGGAATATGGTTC 1200
 QY 1132 AGTTCTTGGGCCAAAGTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAAGCC 1191

Db 1201 AGTTCGTGGGCAAAAGTCAGCCCTGTATGACGTTGATTTCAATCTAGGGCTTGGGAAGCCC 1260
 QY 1192 GAGACTGTGAGAGCGGCAATCTTTGAGCCTGTGAGAGCTTGATGTACTTTATGCCCAAG 1251
 Db 1261 AAGAGTGTACGAGCGGCGGCTTCATTTCCCTTGAGAGCTAATATATTTATGCTAGA 1320
 QY 1252 AAGCCTGATGGGAGTCTGTGTGGCGCTTTCTCTGAGGGATGAGATATGACCGATGG 1311
 Db 1321 TCCTCCAGAGGTGAATGTGGTGTCTTTGCTTTAGAGATAAAGATTGGGAGTGCCTG 1380
 QY 1312 AAGCGGATAGAGAGTGGACCAAGTATGC 1340
 Db 1381 AATGCGGATAAAGATGGACAAATTTATGC 1409

RESULT 8

AAF12071
 ID AAF12071 standard; cDNA; 695 BP.
 XX
 AC AAF12071;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Aspergillus oryzae EST SEQ ID NO:4594.

XX Multiple gene expression; filamentous fungal cell; EST;
 KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
 KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
 KW culture condition; environmental stress; spore morphogenesis;
 KW metabolic pathway engineering; catabolic pathway engineering; ss.

OS Aspergillus oryzae.

XX WO200056762-A2.

XX 28-SEP-2000.

XX 22-MAR-2000; 2000WO-US007781.

XX 22-MAR-1999; 99US-00273623.

XX (NOVO) NOVO NORDISK BIOTECH INC.

PA (NOVO) NOVO NORDISK AS.

XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;

XX WPI; 2000-594572/56.

XX Monitoring differential expression of genes in filamentous fungal cells
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a
 PT substrate of expressed sequence tags.

PS Claim 88; Page 1954-1955; 3161pp; English.

XX The present invention describes a method for monitoring differential
 CC expression of genes in a first filamentous fungal (FF) cell relative to
 CC expression of the same genes in one or more second filamentous fungal
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
 CC are used in the methods for monitoring differential expression of genes
 CC in a first filamentous fungal (FF) cell relative to expression of the
 CC same genes in one or more second filamentous fungal cells. Monitoring the
 CC global expression of genes from FF cells allows the production potential
 CC of the microorganisms to be improved. New genes may be discovered,
 CC possible functions of unknown open reading frames can be identified and
 CC gene copy number variation and stability can be monitored. The expression
 CC of genes can be used to study how FF cells adapt to changes in culture
 CC conditions, environmental stress, spore morphogenesis, recombination,
 CC metabolic or catabolic pathway engineering. Using ESTs provides several
 CC advantages over genomic or random cDNA clones including elimination of
 CC redundancy as one spot on an array equals one gene or open reading frame,
 CC and organisation of the microarrays based on function of the gene

CC products to facilitate analysis of the results. AAF07478 to AAF11247
 CC represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents
 CC ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from
 CC Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from
 CC Trichoderma reesei, which are all specifically claimed in the present
 CC invention

SQ Sequence 695 BP; 174 A; 191 C; 156 G; 172 T; 0 U; 2 Other;

Query Match 10.8%; Score 146.2; DB 3; Length 695;

Best Local Similarity 57.5%; Pred. No. 3.4e-35;

Matches 325; Conservative 0; Mismatches 225; Indels 15; Gaps 3;

QY 5 CTTTCAAGATACAGCTCGACACCTTCGGCCAGCTACAGGCTCTCTTCGATCTACACCC 64

Db 109 CATTACATGTAAAGCTGAACTTCTCTGGGTGAGTGCCTGCCCTC---AGGATCTACACG 165

QY 65 AAATCAGTCTCTCTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTTCAGACCT 124

Db 166 AAATCTGCCTCTGCTTTCCGTTT---GATGCTCTCATCTGATCAGGATAGTCAGGACCC 222

QY 125 TCGAGCAAGGTCTTAAAGCGCTTCTCCGAAGCGCTCCCATGGGTTCGAGGCCAGGTCAAAG 184

Db 223 TAGAGATGGCCTCGAAGACTGTCCACCAATTTCCCGTGGGTAGCAGGCCAGATAGTCA 282

QY 185 CCGAGGGCATTAGCGAGGGAACAACAGGAACTTCTCTTATTCGTCCCTTTTGAGGAGCTTC 244

Db 283 GTGAAGGCGAGCAGCACCAACATCTCTGGCACAATTCATGATCAAAAGCACTGGGGAAGACTC 342

QY 245 CTCGTGTTGTAGTGAAGACCTTCGGGATGATCTTCAGCGCCACGATCGAGGGTATGA 304

Db 343 CACCACTGTTGTGAAGACTTCCGTGATGATCCGACGTTCCGACCATGGACGATTGA 402

QY 305 GAAAGCGGGATACCTCTATGGCGATGTTTGACGAGAAACATCATCGCGCCAAAGAACCGT 364

Db 403 GACGCGCGACTTTCCCTTCGGATGTTAGACGAGAACATCATTTGCTCTCGGAAACCT 462

QY 365 TACCTATTGGACCTCGTACTGTCGCCGACGACCCAAAGCCTGTAAATTCATTGACGCTCA 424

Db 463 TGCCAA-----GCCCTGACGAAGATATTATCTACCGCGCTTCTTGTCCAGGCTA 513

QY 425 ACTTCATCAGGGCGGAGCTCATCTCTCACTGTCAACGGACGACGCGTGTCTATGATATGG 484

Db 514 ATTNTATTACGCGCGCGCTGCTCCTCACTCTTTGTGGCCATCATAGACAATGGACATGA 573

QY 485 TAGGCCAAGATCGGTGATCCGCTACTCTCAAGCGGTGCGGTAAACGACCCCATTCACCG 544

Db 574 CTGGTCANGGACAGGTTATCCACCTTCTCTCGAAGGCATGTCGTGGGGATACATATACAA 633

QY 545 AAGAGAAATGACGCCCATGAACCT 569

Db 634 GATTGAGCTAGAGTCAGGGAACCT 658

RESULT 9

ABZ54817

ID ABZ54817 standard; cDNA; 482 BP.

XX AC ABZ54817;

XX DT 28-MAR-2003 (first entry)

DE Aspergillus oryzae polynucleotide SEQ ID NO 3930.

KW Aspergillus oryzae; fermentation; fungus; industrial; EST;

XX expressed sequence tag; gene; ss.

OS Aspergillus oryzae.

XX WO200279476-A1.

XX 10-OCT-2002.

XX

Db 449 RMASKYK- ---WMRMRWRKKKCSRTTMMGKTGGWMTNGRCRYKKRSKMKGKCRRRR 504

Qy 1203 ACGGCCAATCTTTGAGCCTGTGTGAGAGCTTGATGTACTTTATGCACCAAGAAGCCCTGATGG 1262
: : : : : : | : : : : : : | : : : : : : | : : : : : : | : : : : : :
Db 505 WGRMYRWKRKYMSARYTWRYCARKEYSYSAARKARCWYRGKYIWAGMMWKYKEMYM 564

Qy 1263 CGAGTTCGTGCGCGCGCTTCTCTGAGGGATGAGGATATGGACCGATTGAAGCGCGGATAA 1322
: : : : : : | : : : : : : | : : : : : : | : : : : : : | : : : : : :
Db 565 YKMMWWTKRYSKSWTKCMYSYASCMKSARKAKAGMKCKRSKMSAWSKMSRSSRKCKCA 624

Qy 1323 GGAGTGACCACAAGTATGCGCAGTAGCTT 1350
: : : : : : | : : : : : : | : : : : : : | : : : : : : | : : : : : :
Db 625 SKRSSAKRYAMMGWMTSGSRMSRWKSYT 652

RESULT 11
ADA71938/c
ID ADA71938 standard; DNA; 2000 BP.
XX AC ADA71938;
XX CC
XX DT 20-NOV-2003 (first entry)
XX DE Rice gene, SEQ ID 5263.
XX Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX Oryza sativa.
XX WO2003000898-A1.
XX
XX PD 03-JAN-2003.
XX PF 22-JUN-2001; 2001WO-IB001105.
XX PR 22-JUN-2001; 2001WO-IB001105.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PA Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX DR WPI; 2003-175290/17.
XX PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX Claim 27; SEQ ID NO 5263; 899pp; English.
XX The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC the expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.

XX SQ Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

Query Match 3.0%; Score 40.2; DB 8; Length 2000;
Best Local Similarity 9.2%; Pred. No. 0.22;
Matches 55; Conservative 287; Mismatches 255; Indels 4; Gaps 3;

Qy 165 GGTCCGAGGCCAGGTCAAAGCGGCGCATTAAGCAGGAAACACAGGAATCTCTTTAT 224
: : : : : : | : : : : : : | : : : : : : | : : : : : : | : : : : : :
Db 706 KRSYRRRWYKRGWTYRVRYWRSCTRMRNRKRKRWAGSMKSCMWYWRGARSWMY 647

Qy	225	CGTCCCTTTGAGAGCGTTCTCGTGTGTAGTGAAGACCTCCGGATGATCCCTTCAGC	28
Db	646	SKYCSAKCKKTRYM--TSSYMTSGMYGMTYSYKSMWNTSKVSYNGKMTCTMYTSMKGS	589
Qy	285	GCCACAGATCGAGGGTATGAGAAAGG-CGGGATACCCTATGCGGATGTTTTCAGCAGAACA	343
Db	588	TRRSKMGWSGSRMYMKWRKVRKVRMYKWKCTWRRCMYRWGYTMYTTSRSRMVY	529
Qy	344	TCATCGCGCCCAAGGAAGCGTTTACCTATTGGAACCTGGTACTGGTCCGACGACCCAAAGC	403
Db	528	TGRYKARYTSKRRYMWYKRYKVCWYYYGYMWYKCSYMMRYGYCKACKCCYAMCWKAAYS	469
Qy	404	CTGTAATTCTATTGACAGCTCAACTTCATCAAGGGCGGACTCATCTCTCATCTGTCACGGAC	463
Db	468	GMMYMYRYKYSKWRMRMSTKYMWMSMYKKCRSMKYGAKGCYGCWMYTCYSGYMKWYTMG	409
Qy	464	AGCACGGTGCTATGGATATGGTAGGCCAAGATGCGGTGATCGGTCTACTCTCCAAGCGT	523
Db	408	SYKSRCYKMYRMWYKGMWYMYSAYSMMTWYTYTAKYWKYWKRRGTMSWYKSYK	349
Qy	524	GCCGTAAACGACCCATTACCCGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGACGA	583
Db	348	KKYCTWCYMKCMR-CYEWKRMKKTKYKRCYCWRYATCYWCCYKRGWYSRSMR	250
Qy	584	TAGTTCCTTACTGTAAACTATACGATTGGCCCGGAGTAGATCATCATGATGTCACAAAG	643
Db	289	TAGKWKMSWSRWCRSYWKYKMYKMWKKSYYMSYGMARSSGTWRSAAKRTYKGYSTSR	230
Qy	644	CTGATGTAGCTGGTGGTGACGCTGTTCTCACGCCGGTCAGTCAAGCTGGGCGTCTCTCA	703
Db	229	RAKWMRACRMYSACRRYSRTSYCCSCYCGSKWYMSKCSMRMTCSWCSCCYTCYYG	170
Qy	704	CATTACGCCCAAGCCCATGTACAGAGCTCAAGATGCTGCTACCAAGACTCTTGACGCGAT	763
Db	169	AMCWSCCSMYMGSCGYCTRGWKRSKYSMCKKYCSCTKYCSYGYRYCKWKYKSY	110
Qy	764	C 764	
Db	109	Y 109	
RESULT 12			
ID	AD181367		
XX	AD181367 standard; DNA; 663 BP.		
AC	AD181367;		
DT	22-APR-2004 (first entry)		
XX	M. tuberculosis VNTR locus Mtb-v18 nucleotide sequence.		
DE	valuable number tandem repeat; VNTR; Mycobacterium tuberculosis;		
KW	detection; tuberculosis; gene; ds.		
XX	Mycobacterium tuberculosis.		
XX	WO2004009837-A2.		
XX	29-JAN-2004.		
XX	21-JUL-2003; 2003WO-US022950.		
XX	19-JUL-2002; 2002US-0397224P.		
XX	(UYAR-) UNIV ARIZONA.		
PA	(KEIM/) KEIM P S.		
PA	(SCHU/) SCHUPP J M.		
PA	(SPUR/) SPURGIESZ R S.		
XX	Keim PS, Schupp JM, Spurgiesz RS;		
PI	WPI; 2004-123400/12.		
XX			

PT New isolated nucleic acid, useful for detecting Mycobacterium
PT tuberculosis species in assays employing probes, including a
XX nanodetection device.

PS Example 8; Page 24-25; 44pp; English.

XX The present invention describes an isolated nucleic acid (I) comprising
CC at least 12 consecutive nucleotides of a nucleotide sequence selected
CC from the 18 sequences of SEQ ID NO: 1-18 (AD181342 to AD181359) or the
CC complementary sequences of SEQ ID NO: 1-18. Also described: (1) a pair of
CC forward and reverse primers for amplification of valuable number tandem
CC repeats (VNTR) located in DNA isolated from Mycobacterium tuberculosis
CC species, where the pair is selected from SEQ ID NO: 1 and 2; SEQ ID NO: 3
CC and 4; SEQ ID NO: 5 and 6; SEQ ID NO: 7 and 8; SEQ ID NO: 9 and 10; SEQ
CC ID NO: 11 and 12; SEQ ID NO: 13 and 14; SEQ ID NO: 15 and 16 or SEQ ID
CC NO: 17 and 18; (2) a method for detecting a M. tuberculosis species; (3)
CC a kit for the detection of a M. tuberculosis species comprising: (a) the
CC pair of forward and reverse primers; (b) nucleic acids having an
CC observable marker; (c) a transcriptase; and (d) buffers and salts
CC suitable for causing polymerisation of VNTR in DNA from the M.
CC tuberculosis species in a polymerase chain reaction (PCR); and (4) a
CC method of sub-typing a M. tuberculosis strain. The pair of forward and
CC reverse primers are useful as PCR primers in the detection of M.
CC tuberculosis species. The kit is useful for multiplexing DNA from a M.
CC tuberculosis species, where the kit comprises mixtures of the pair of
CC forward and reverse primers for use in a multiplex instrument. The
CC nucleic acid is useful for detecting M. tuberculosis species in assays
CC employing probes, including a nanodetection device. The sub-typing scheme
CC is useful for the epidemiological study of M. tuberculosis and may be
CC applied to the local detection of the pathological causative agent of
CC tuberculosis. The present sequence represents a M. tuberculosis VNTR
CC locus MtB-v18 nucleotide sequence, which is used in an example from the
XX present invention.

SQ Sequence 663 BP; 135 A; 208 C; 213 G; 107 T; 0 U; 0 Other;

Query Match 2.9%; Score 39.8; DB 12; Length 663;
Best Local Similarity 49.8%; Pred. No. 0.16;
Matches 101; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
QY 956 TCGGCGAATGCCAACGAGTCACTCGCGCAACAGCATCAGCGCTTCTTCAGAACTCG 1015
DB 433 TCGAGAGGTTTCGCGCGCCCGCCCACTCGAGAGCGGCAATCGGCTACCGGATATCC 492
QY 1016 ACCCGCGAGCATGCGCGCAACAGAGGTCTCGCGACGTACTGCAACAACACCCCG 1075
DB 493 AGCCACCAAGCATCCGCAACTCGAGATGTTCTGCCCCGNACTGCGGAGGAGCTCG 552
QY 1076 ACAAGTCCAAAGTATCCCTGACGGTGTATGCGGACCCATCTACCGAGCTATGCTGAGTT 1135
DB 553 ACCGGCTTACCTGCGTTCAACGAGGACGCGTGCCTTCGACGCGGAGTTGCGCATTTG 612
QY 1136 CTGGCGCAAGTGGGACTCTGG 1158
DB 613 CCAGGCACAGCTGTGCGCTGG 635

RESULT 13

AAI99682_42
Continuation (43 of 45) of AAI99682 from base 4200001 (Mycobacterium tuberculosis strain
WP Sequence split into 45 fragments LOCUS AAI99682 Accession AAI99682

WP	Fragment Name	Begin	End
WP	AAI99682_00	1	110000
WP	AAI99682_01	100001	210000
WP	AAI99682_02	200001	310000
WP	AAI99682_03	300001	410000
WP	AAI99682_04	400001	510000
WP	AAI99682_05	500001	610000
WP	AAI99682_06	600001	710000
WP	AAI99682_07	700001	810000
WP	AAI99682_08	800001	910000
WP	AAI99682_09	900001	1010000
WP	AAI99682_10	1000001	1110000

WP	AAI99682_11	1100001	1210000
WP	AAI99682_12	1200001	1310000
WP	AAI99682_13	1300001	1410000
WP	AAI99682_14	1400001	1510000
WP	AAI99682_15	1500001	1610000
WP	AAI99682_16	1600001	1710000
WP	AAI99682_17	1700001	1810000
WP	AAI99682_18	1800001	1910000
WP	AAI99682_19	1900001	2010000
WP	AAI99682_20	2000001	2110000
WP	AAI99682_21	2100001	2210000
WP	AAI99682_22	2200001	2310000
WP	AAI99682_23	2300001	2410000
WP	AAI99682_24	2400001	2510000
WP	AAI99682_25	2500001	2610000
WP	AAI99682_26	2600001	2710000
WP	AAI99682_27	2700001	2810000
WP	AAI99682_28	2800001	2910000
WP	AAI99682_29	2900001	3010000
WP	AAI99682_30	3000001	3110000
WP	AAI99682_31	3100001	3210000
WP	AAI99682_32	3200001	3310000
WP	AAI99682_33	3300001	3410000
WP	AAI99682_34	3400001	3510000
WP	AAI99682_35	3500001	3610000
WP	AAI99682_36	3600001	3710000
WP	AAI99682_37	3700001	3810000
WP	AAI99682_38	3800001	3910000
WP	AAI99682_39	3900001	4010000
WP	AAI99682_40	4000001	4110000
WP	AAI99682_41	4100001	4210000
WP	AAI99682_42	4200001	4310000
WP	AAI99682_43	4300001	4410000
WP	AAI99682_44	4400001	4411529

Query Match 2.9%;

Best Local Similarity 49.8%; Score 39.8; DB 4; Length 110000;

Pred. No. 2.4;

Matches 101; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY	956 TCGGCGAATGCCAACGAGTCACTCGCGCAACAGCATCAGCGCTTCTTCAGAACTCG 1015
DB	27170 TCGAGAGGTTTCGCGCGCCCGCCCACTCGAGAGCGGCAATCGGCTACCGGATATCC 27229
QY	1016 ACCCGCGAGCATGCGCGCAACAGAGGTCTCGCGACGTACTGCAACAACACCCCG 1075
DB	27230 AGCCACCAAGCATCCGCAACTCGAAGATGTTCTGCCCCGNACTGCGGAGGAGCTCG 27289
QY	1076 ACAAGTCCAAAGTATCCCTGACGGTGTATGCGGACCCATCTACCGAGCTATGCTGAGTT 1135
DB	27290 ACCGGCTTACCTGCGTTCAACGAGGACGCGTGCCTTCGAGACGCGGAGTTGCGCATTTG 27349
QY	1136 CTGGCGCAAGTGGGACTCTGG 1158
DB	27350 CCAGGCACAGCTGTGCGCTGG 27372

RESULT 14

AAI99683_42

Continuation (43 of 44) of AAI99683 from base 4200001 (Mycobacterium tuberculosis strain
WP Sequence split into 44 fragments LOCUS AAI99683 Accession AAI99683

WP	Fragment Name	Begin	End
WP	AAI99683_00	1	110000
WP	AAI99683_01	100001	210000
WP	AAI99683_02	200001	310000
WP	AAI99683_03	300001	410000
WP	AAI99683_04	400001	510000
WP	AAI99683_05	500001	610000
WP	AAI99683_06	600001	710000
WP	AAI99683_07	700001	810000
WP	AAI99683_08	800001	910000
WP	AAI99683_09	900001	1010000
WP	AAI99683_10	1000001	1110000
WP	AAI99683_11	1100001	1210000

```
WP AA199683_12 1200001 1310000
WP AA199683_13 1300001 1410000
WP AA199683_14 1400001 1510000
WP AA199683_15 1500001 1610000
WP AA199683_16 1600001 1710000
WP AA199683_17 1700001 1810000
WP AA199683_18 1800001 1910000
WP AA199683_19 1900001 2010000
WP AA199683_20 2000001 2110000
WP AA199683_21 2100001 2210000
WP AA199683_22 2200001 2310000
WP AA199683_23 2300001 2410000
WP AA199683_24 2400001 2510000
WP AA199683_25 2500001 2610000
WP AA199683_26 2600001 2710000
WP AA199683_27 2700001 2810000
WP AA199683_28 2800001 2910000
WP AA199683_29 2900001 3010000
WP AA199683_30 3000001 3110000
WP AA199683_31 3100001 3210000
WP AA199683_32 3200001 3310000
WP AA199683_33 3300001 3410000
WP AA199683_34 3400001 3510000
WP AA199683_35 3500001 3610000
WP AA199683_36 3600001 3710000
WP AA199683_37 3700001 3810000
WP AA199683_38 3800001 3910000
WP AA199683_39 3900001 4010000
WP AA199683_40 4000001 4110000
WP AA199683_41 4100001 4210000
WP AA199683_42 4200001 4310000
WP AA199683_43 4300001 4403765

Query Match 2.9%; Score 39.8; DB 4; Length 110000;
Best Local Similarity 49.8%; Pred. No. 2.4;
Matches 101; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 956 TCGGCGAATCGCAACGAGTCACTCGGCGCAACAGCATCACGCCCTTGGTTGAGAACTCG 1015
Db 19416 TCGAGGAGGTTCGCGCGCCCACTCGACGAGCGCAATCGGCTACGCGATATCC 19475

QY 1016 ACCCGCGAGCATCGCCGCGCAACAGAGGTCTCGGAGCTACTCGACACCAACCCCG 1075
Db 19476 ACGCCACCGAGTACCGCGAACTCGAAGATGTTCTGCGCCCGGAACATGCGGAGGACTCG 19535

QY 1076 ACAAGTCCAACTGATCCCTGACCGGTGATCGCGGACCATCTACCAGCGTCACTGCTGAGTT 1135
Db 19536 ACGGCTTACCTGCGGTTCAACGAGAGCGCGCTGCGGAGCGGAGTTGCGCATTTG 19595

QY 1136 CTTGGGCCAAGTGGGACTCTGG 1158
Db 19596 CCCAGGCACAGCTGTTGCGGCTGG 19618

RESULT 15
AAT37310
ID AAT37310 standard; cDNA to mRNA; 1605 BP.
XX AC
XX AAT37310;
XX AC
XX AAT37310;
DT 16-OCT-2003 (revised)
DT 06-FEB-1997 (first entry)
XX Aromatic acyl transferase coding sequence.
XX Aromatic acyl transferase; transformation; anthocyanin pigment; plants;
XX acylation; colour; tone; colouration; colour change; Gentiana triflora;
XX Petunia hybrida; Perilla ocimoides; Senecio cruentus;
XX Lavandula angustifolia; ds.
XX OS Petunia x hybrida; (Clone pPAT48).
XX FH Key Location/Qualifiers
```

```
FT CDS 67.1413
FT FT /*tag= a
XX PN /product= "Aromatic acyl transferase."
XX WO9625500-A1.
XX PD 22-AUG-1996.
XX PF 16-FEB-1996; 96WO-JP000348.
XX PR 17-FEB-1995; 95JP-00067159.
XX PR 29-JUN-1995; 95JP-00196915.
XX PR 30-JAN-1996; 96JP-00046534.
XX (SUNR ) SUNTORY LTD.
XX Ashikari T, Tanaka Y, Fujiwara H, Nakao M, Fukui Y, Yonekura K;
XX Mizutani M, Kusumi T;
XX WPI; 1996-393401/39.
XX P-PSDB; AAW04724.
XX DNA coding for aromatic acyl transferase - for transforming plants which
XX produce anthocyanin pigments and thus altering colour tone, e.g. of
XX flowers.
XX Claim 4; Page 61-65; 94pp; Japanese.
XX Vectors containing DNA fragments encoding proteins of plant origin with
XX aromatic acyl transferase activity may be used to transform plants which
XX produce anthocyanin pigments. The aromatic acyl transferase acylates the
XX pigments in the flower resulting in colour tone changes and allowing new
XX colourations to be produced. Six specific DNA sequences encoding aromatic
XX acyl transferase from different plants are described in AAT37308-T37313.
XX (Updated on 16-OCT-2003 to standardise OS field)
XX SQ Sequence 1605 BP; 477 A; 319 C; 375 G; 434 T; 0 U; 0 Other;

Query Match 2.7%; Score 36.4; DB 2; Length 1605;
Best Local Similarity 51.9%; Pred. No. 3.1;
Matches 107; Conservative 0; Mismatches 96; Indels 3; Gaps 1;

QY 1154 TCTGGGATTACGACTTTGGGCTCGGACTGGGTAAAGCCCGAGACTGTGAGACGCCAATCT 1213
Db 1217 TCAAGGTTTACGACGCTGGATTTTGGATGGGGAAGCCAGAGAGTGTGAGAGTGGTTCGA 1276

QY 1214 TTGAGCCTCTTCGAGAGCTTGTATGTTTATGC---CCAAGAAGCCTGATGCGAGTTCT 1270
Db 1277 ACAATAGTTTGTATGGAATGGTGTATTGTACCAAGGCAAAATGAGGAGGAGCATTC 1336

QY 1271 GTGCGCGCTTTCTCTGAGGGATGAGGATATGACCGGATTTGAAGCGGATAAGGAGTGA 1330
Db 1337 ATGTGGAGATTAGTTTGGAAAGCAAAATGCTATGAGAGGTTTGGAGAAAGATAAAGAGTTCC 1396

QY 1331 CCAAGTATCGGACGATACGTTGGTTAG 1356
Db 1397 TCATGGAACACTGCTTAATTTGCTTAG 1422
```

Search completed: January 23, 2005, 14:47:30

Job time : 737 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 21:45:08 ; Search time 6029 Seconds
(without alignments)
10636.064 Million cell updates/sec

Title: US-10-614-954-5
Perfect score: 1356
Sequence: 1 atggtttcaagatacagct.....atgcgcagtaactgttgtag 1356

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1356	100.0	1356	6	BD247864 Transgeni
2	1356	100.0	1356	6	AR193433 Sequence
3	1356	100.0	1356	6	AR430218 Sequence
4	1340	98.8	1605	6	E31785 Trichothec
5	1340	98.8	1605	8	AB000874 Gibberell
6	1340	98.8	3003	8	AB009607 Gibberell
7	1340	98.8	8646	8	AB011417 Gibberell
8	1334	98.4	1336	8	AF212605 Gibberell
9	1334	98.4	1336	8	AF212608 Gibberell
10	1330.8	98.1	1336	8	AF212603 Gibberell
11	1330.8	98.1	1336	8	AF212606 Gibberell
12	1330.8	98.1	1336	8	AF212607 Gibberell
13	1329.2	98.0	1336	8	AF212602 Gibberell
14	1329.2	98.0	1336	8	AF212604 Gibberell
15	1329	98.0	1329	8	AY452807 Gibberell
16	1329	98.0	1329	8	AY452808 Gibberell
17	1321.2	97.4	1336	8	AF212582 Gibberell
18	1321.2	97.4	1336	8	AF212583 Gibberell
19	1321.2	97.4	1336	8	AF212584 Gibberell

20	1321.2	97.4	1336	8	AF212585	AF212585 Gibberell
21	1321.2	97.4	1336	8	AF212586	AF212586 Gibberell
22	1321.2	97.4	1336	8	AF212587	AF212587 Gibberell
23	1319.6	97.3	1336	8	AF212594	AF212594 Gibberell
24	1319.6	97.3	1336	8	AF212601	AF212601 Gibberell
25	1318	97.2	1336	8	AF212595	AF212595 Gibberell
26	1318	97.2	1336	8	AF212596	AF212596 Gibberell
27	1318	97.2	1336	8	AF212597	AF212597 Gibberell
28	1318	97.2	1336	8	AF212598	AF212598 Gibberell
29	1318	97.2	1336	8	AF212599	AF212599 Gibberell
30	1318	97.2	1336	8	AF212600	AF212600 Gibberell
31	1316.4	97.1	1336	8	AF212588	AF212588 Gibberell
32	1314.8	97.0	1326	8	AY452813	AY452813 Fusarium
33	1314.8	97.0	1326	8	AY452814	AY452814 Fusarium
34	1314.8	97.0	1336	8	AF212589	AF212589 Gibberell
35	1310	96.6	1326	8	AY452810	AY452810 Fusarium
36	1310	96.6	1326	8	AY452811	AY452811 Fusarium
37	1310	96.6	1326	8	AY452812	AY452812 Fusarium
38	1304.4	96.2	1322	8	AY222842	AY222842 Gibberell
39	1304.4	96.2	1322	8	AY222882	AY222882 Gibberell
40	1303.6	96.1	1336	8	AF212590	AF212590 Gibberell
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ALIGNMENTS

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BD247864
LOCUS BD247864 1356 bp DNA linear PAT 17-JUL-2003
DEFINITION Transgenic plant and methods.
ACCESSION BD247864
VERSION BD247864.1 GI:33057634
KEYWORDS JP 2002540787-A/4.
SOURCE Gibberella zeae
ORGANISM Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 1356)
AUTHORS Hohn,T.M., Peters,C., Salmeron,J.M., Janet, Reed,N. and Dawson,J.L.
TITLE Transgenic plant and methods
JOURNAL Patent: JP 2002540787-A 4 03-DEC-2002;
SYNGENTA PARTICIPATIONS AG
COMMENT OS Fusarium graminearum
PN JP 2002540787-A/4
PF 03-DEC-2002
PR 29-MAR-2000 JP 2000609553
PR 31-MAR-1999 US 09/282995,11-FEB-2000 US 09/502852 PI
THOMAS M HOHN,CHERYL PETERS,JOHN MANUEL SALMERON,JANET PI N
REED,JOHN L DAWSON
PC C12N15/09,A01H5/00,C12N1/15,C12N5/10//C12N1/15,C12R1:645), PC
(C12N5/10,C12R1:91),C12N15/00,C12N5/00,C12N5/00,C12R1:91) CC
Transgenic plant and methods
FH Key Location/Qualifiers
FT source 1. 1356
FT /organism='Fusarium graminearum'.
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Sequence 5 from patent US 6346655.
DEFINITION AR193433
ACCESSION AR193433
VERSION AR193433.1 GI:20239398
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1356)
AUTHORS Hohn,T.M., Peters,C. and Salmeron,J.
TITLE Trichothecene-Resistant transgenic plants
JOURNAL Patent: US 6346655-A 5 12-FEB-2002;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	1261	GCGAGTTCTGTGCGGCTTTCTCTGAGGGATGAGGATGAGACCGATTGAAGGCGGAT	1320
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DEFINITION	Sequence 5 from patent US 6646184.		
ACCESSION	AR430218		
VERSION	AR430218.1		
KEYWORDS	GI:40190948		
SOURCE	Unknown.		
ORGANISM	Unknown.		
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RESULT 4

E31785
 LOCUS 1605 bp DNA linear PAT 18-JUN-2001
 DEFINITION Trichothecene 3-O-acetyltransferase gene.
 ACCESSION E31785
 VERSION E31785.1 GI:13018619
 KEYWORDS JP 2000032985-A/1.
 SOURCE Gibberella zeae
 ORGANISM
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 1 (bases 1 to 1605)
 Isamu, Y., Makoto, K., Akira, T., Hiroyuki, K. and Katsumi, Y.
 Trichothecene 3-O-acetyltransferase gene
 Patent: JP 2000032985-A 1 02-FEB-2000;
 RIKAKU KENKYUSHO, ISAMU YAMAGUCHI
 OS Fusarium graminearum
 PN JP 2000032985-A/1
 PD 02-FEB-2000
 PF 15-JUL-1998 JP 1998200280
 PR ISAMU YAMAGUCHI, MAKOTO KIMURA, AKIRA TAKATSUKI, HIROYUKI
 KOSHINO, PI KATSUMI YONEYAMA
 PC C12N15/09, A01H5/00, A01N63/00, C12N1/21, C12N5/10, C12N9/10// PC
 (C12N15/09, C12R1:77), (C12N1/21, C12R1:19), (C12N5/10, C12R1:91), PC
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 FH Key Location/Qualifiers
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LOCUS Gibberella zeae mRNA for trichothecene 3-O-acetyltransferase, 1605 bp mRNA linear PLN 21-JAN-1998
DEFINITION complete cds.
ACCESSION AB000874
VERSION AB000874.1 GI:2804249
KEYWORDS trichothecene 3-O-acetyltransferase.
SOURCE Gibberella zeae
ORGANISM Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
AUTHORS Kimura,M., Kaneko,I., Komiyama,M., Takatsuki,A., Koshino,H.,
Yoneyama,K. and Yamaguchi,I.
TITLE Trichothecene 3-O-acetyltransferase protects both the producing
organism and transformed yeast from related mycotoxins. Cloning and
characterization of Tril01
J. Biol. Chem. 273 (3), 1654-1661 (1998)
98104153
9430709
PUBMED 2 (bases 1 to 1605)
AUTHORS Kimura,M.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-1997) Makoto Kimura, The Institute of Physical
and Chemical Research (RIKEN), Microbial Toxicology Laboratory,
Hiroshima 2-1, Wako, Saitama 351-01, Japan
(E-mail:mkimura@postman.riken.go.jp, Tel:81-048-467-9518,
Fax:81-048-462-4676)
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Query Match 98.8%; Score 1340; DB 8; Length 1605;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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VERSION AF212605.1 GI:12003706
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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O'Donnell, K., Kistler, H. C., Tacke, B. K. and Casper, H. H.
Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of Fusarium graminearum, the
fungus causing wheat scab
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
JOURNAL
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PUBMED 10869425
REFERENCE
2 (bases 1 to 1336)
O'Donnell, K.
Direct Submission
AUTHORS
Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USA, 1815 N. University St., Peoria, IL 61604, USA
JOURNAL
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Best Local Similarity 100.0%; Pred. No. 0;
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DEFINITION 3-O-acetyltransferase, partial cds.
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VERSION AF212608.1 GI:12003712
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 1336)
O'Donnell K., Kistler, H. C., Tacke, B. K. and Casper, H. H.
AUTHORS Gene genealogies reveal global phylogeographic structure and
TITLE reproductive isolation among lineages of *Fusarium graminearum*, the
fungus causing wheat scab
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
JOURNAL
MEDLINE 20345085
PUBMED 10869425
REFERENCE 2 (bases 1 to 1336)
O'Donnell, K.
AUTHORS Direct Submission
TITLE Submitted (08-DEC-1999) Microbial Properties Research,
JOURNAL NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 1336)
AUTHORS O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
TITLE Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of Fusarium graminearum, the
fungus causing wheat scab
PROC. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
MEDLINE 20345085
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REFERENCE 2 (bases 1 to 1336)
AUTHORS O'Donnell, K.
TITLE Direct Submission
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NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
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DEFINITION 3-O-acetyltransferase, partial cds.
ACCESSION AF212606
VERSION AF212606.1 GI:12003708
KEYWORDS Gibberella zeae
SOURCE Gibberella zeae
ORGANISM Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 1336)
O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of *Fusarium graminearum*, the
fungus causing wheat scab
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
MEDLINE 20345085
PUBMED 10869425
REFERENCE 2 (bases 1 to 1336)
O'Donnell, K.
Direct Submission
Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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LOCUS Gibberella zeae strain NRRL28439 trichothecene
DEFINITION 3-O-acetyltransferase, partial cds.
ACCESSION AF212607
VERSION AF212607.1 GI:12003710
KEYWORDS
SOURCE Gibberella zeae
ORGANISM Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 1336)
O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
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fungus causing wheat scab
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
20345085
10869425
REFERENCE 2 (bases 1 to 1336)
O'Donnell, K.
Direct Submission
Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
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Query Match 98.1%; Score 1330.8; DB 8; Length 1336;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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3-O-acetyltransferase, partial cds.
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE
1. (bases 1 to 1336)
O'Donnell, K., Kistler, H. C., Tacke, B. K. and Casper, H. H.
Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of *Fusarium graminearum*, the
fungus causing wheat scab
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
JOURNAL
MEDLINE
20345085
PUBMED
10869425
REFERENCE
2. (bases 1 to 1336)
O'Donnell, K.
Direct Submission
TITLE
Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USA, 1815 N. University St., Peoria, IL 61604, USA
JOURNAL
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ORIGIN

Query Match 98.0%; Score 1329.2; DB 8; Length 1336;
Best Local Similarity 99.8%; Pred. No. 0;
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DEFINITION	Gibberella zeae strain NRRL1338; trichothecene 3-O-acetyltransferase, partial cds.		
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VERSION	AF212604.1	GI:12003704	
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SOURCE	Gibberella zeae		
ORGANISM	Gibberella zeae		
REFERENCE	1 (bases 1 to 1336)		
AUTHORS	O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.		
TITLE	Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of Fusarium graminearum, the fungus causing wheat scab		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)		
MEDLINE	20345085		
PUBMED	10869425		
REFERENCE	2 (bases 1 to 1336)		
AUTHORS	O'Donnell, K.		
TITLE	Direct Submission		
JOURNAL	Submitted (08-DEC-1999) Microbial Properties Research, NCAUR-ARS-USA, 1815 N. University St., Peoria, IL 61604, USA		
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trichothecene-3-O-acetyltransferase gene, partial cds.

ACCESSION
AY452807

VERSION
AY452807.1

KEYWORDS
GI:48527666

SOURCE
Gibberella zeae (anamorph: Fusarium graminearum)

ORGANISM
Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE
1 (bases 1 to 1329)
O'Donnell, K., Ward, T.J., Geiser, D.M., Corby Kistler, H. and Aoki, T.
Genetical concordance between the mating type locus and seven
other nuclear genes supports formal recognition of nine
phylogenetically distinct species within the Fusarium graminearum
clade

AUTHORS
O'Donnell, K., Ward, T.J., Geiser, D.M., Corby Kistler, H. and Aoki, T.

TITLE
Genetical concordance between the mating type locus and seven
other nuclear genes supports formal recognition of nine
phylogenetically distinct species within the Fusarium graminearum
clade

JOURNAL
Fungal Genet. Biol. 41 (6), 600-623 (2004)

PUBMED
15121083

REVIEWED
2 (bases 1 to 1329)

AUTHORS
O'Donnell, K.

TITLE
Direct Submission

JOURNAL
Submitted (29-OCT-2003) Microbial Genomics, USDA, ARS, 1815 N.
University St., Peoria, IL 61604, USA

FEATURES
Location/Qualifiers

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RT "Trichothecene 3-O-acetyltransferase protects both the producing organism and transformed yeast from related mycotoxins. Cloning and characterization of."
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RT "The mystery of the trichothecene 3-O-acetyltransferase gene. Analysis of the region around Tri101 and characterization of its homologue from Fusarium sporotrichioides."
RL FEBS Lett. 435:163-168(1998).
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Db 1 MAFKIQDLTGLQPLGILLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60
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Db 61 KAEIGSEGNTGTSFIVPFEDVRVVKDLRDDPSAPTTIEGMRKAGYPMAMFENIIAPRK 120
Qy 121 TLPFGTGTGDDPKPVLILQNLFIKGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180
Db 121 TLPFGTGTGDDPKPVLILQNLFIKGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180
Qy 181 TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGDAVLTPVSASWAFKFSKA 240
Db 181 TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGDAVLTPVSASWAFKFSKA 240
Qy 241 MSELKDAATKTLDASTKFKVSTDDALSAFIWKSASRVRLERIDGSAPTFCRAVDARPAWG 300
Db 241 MSELKDAATKTLDASTKFKVSTDDALSAFIWKSASRVRLERIDGSAPTFCRAVDARPAWG 300
Qy 301 VSNYPGLQNMVTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLNHNPKD 360
Db 301 VSNYPGLQNMVTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLNHNPKD 360
Qy 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEFVESLMYFMPKPKD 420
Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEFVESLMYFMPKPKD 420
Qy 421 GEFCALSLRDEDMRLKADKEWT 444
Db 421 GEFCALSLRDEDMRLKADKEWT 444

RESULT 2

Q9HDE2 ID Q9HDE2 PRELIMINARY; PRT; 444 AA.
AC Q9HDE2;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Trichothecene 3-O-acetyltransferase (Fragment).
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL29169, and NRRL28063;
RX MEDLINE=20345085; PubMed=10869425;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of Fusarium graminearum, the fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910(2000).
DR EMBL; AF212608; AAG43715.1; -;
DR EMBL; AF212605; AAG43712.1; -;
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Transferase.
FT NON TER
SQ SEQUENCE 444 444 EBCD4ABE2BASF8F5 CRC64;
Query Match 98.4%; Score 2296; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.6e-162;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFKIQDLTGLQPLGILLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60
Db 1 MAFKIQDLTGLQPLGILLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60
Qy 61 KAEIGSEGNTGTSFIVPFEDVRVVKDLRDDPSAPTTIEGMRKAGYPMAMFENIIAPRK 120
Db 61 KAEIGSEGNTGTSFIVPFEDVRVVKDLRDDPSAPTTIEGMRKAGYPMAMFENIIAPRK 120

Qy 121 TLPFGTGTGDDPKPVLILQNLFIKGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180
Db 121 TLPFGTGTGDDPKPVLILQNLFIKGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180
Qy 181 TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGDAVLTPVSASWAFKFSKA 240
Db 181 TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGDAVLTPVSASWAFKFSKA 240
Qy 241 MSELKDAATKTLDASTKFKVSTDDALSAFIWKSASRVRLERIDGSAPTFCRAVDARPAWG 300
Db 241 MSELKDAATKTLDASTKFKVSTDDALSAFIWKSASRVRLERIDGSAPTFCRAVDARPAWG 300
Qy 301 VSNYPGLQNMVTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLNHNPKD 360
Db 301 VSNYPGLQNMVTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLNHNPKD 360
Qy 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEFVESLMYFMPKPKD 420
Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEFVESLMYFMPKPKD 420
Qy 421 GEFCALSLRDEDMRLKADKEWT 444
Db 421 GEFCALSLRDEDMRLKADKEWT 444

RESULT 3

Q9HDE5 ID Q9HDE5 PRELIMINARY; PRT; 444 AA.
AC Q9HDE5;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Trichothecene 3-O-acetyltransferase (Fragment).
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL28336, NRRL5883, NRRL6394, and NRRL13383;
RX MEDLINE=20345085; PubMed=10869425;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of Fusarium graminearum, the fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910(2000).
DR EMBL; AF212606; AAG43713.1; -;
DR EMBL; AF212602; AAG43709.1; -;
DR EMBL; AF212603; AAG43710.1; -;
DR EMBL; AF212604; AAG43711.1; -;
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Transferase.
FT NON TER
SQ SEQUENCE 444 444 E2233359B5D4A800 CRC64;

Query Match 98.2%; Score 2291; DB 2; Length 444;
Best Local Similarity 99.8%; Pred. No. 3.9e-162;
Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAFKIQDLTGLQPLGILLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60
Db 1 MAFKIQDLTGLQPLGILLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60
Qy 61 KAEIGSEGNTGTSFIVPFEDVRVVKDLRDDPSAPTTIEGMRKAGYPMAMFENIIAPRK 120
Db 61 KAEIGSEGNTGTSFIVPFEDVRVVKDLRDDPSAPTTIEGMRKAGYPMAMFENIIAPRK 120
Qy 121 TLPFGTGTGDDPKPVLILQNLFIKGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180
Db 121 TLPFGTGTGDDPKPVLILQNLFIKGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180

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QY 181 TEEMTAMNLDKTIIVPYLNTYIGPEVDHQIVKADVAGDAVLTPVSASWAFPTSPKA 240
DB 181 TEEMTAMNLDKTIIVPYLNTYIGPEVDHQIVKADVAGDAVLTPVSASWAFPTSPKA 240
QY 241 MSELKDAATKTLDASTKFPVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
DB 241 MSELKDAATKTLDASTKFPVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
QY 301 VSNYPGLLQNMVTHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLNHNPDK 360
DB 301 VSNYPGLLQNMVTHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLNHNPDK 360
QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFPEVSLMYFMPKPKDD 420
DB 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFPEVSLMYFMPKPKDD 420
QY 421 GEFCAALSRLDEDMDLKADKEWT 444
DB 421 GEFCAALSRLDEDMDLKADKEWT 444

RESULT 4
Q6J1Y2 PRELIMINARY; PRT; 442 AA.
AC Q6J1Y2;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 01-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Trichothecene-3-O-acetyltransferase (Fragment)
OS Gibberella zeae (Fusarium graminearum)
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL34079, and NRRL31084;
RX PubMed=15121083;
RA O'Donnell K., Ward T.J., Geiser D.M., Corby Kistler H., Aoki T.;
RT "Genetical concordance between the mating type locus and seven
RT other nuclear genes supports formal recognition of nine
RT phylogenetically distinct species within the Fusarium graminearum
RT clade.";
RL Fungal Genet. Biol. 41:600-623 (2004).
DR EMBL; AY452808; AAT45943.1; -.
DR EMBL; AY452807; AAT45942.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
DR Transferase.
KW 1
FT NON TER 442 442
SQ SEQUENCE 442 AA; 48387 MW; 233AD67C82C4C9AF CRC64;

Query Match
Best Local Similarity 98.0%; Score 2287; DB 2; Length 442;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FKIQDLTGLQGLLSIYTIQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVKA 62
DB 1 FKIQDLTGLQGLLSIYTIQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVKA 60
QY 63 EGISEGNTGTSFIVPPEDVPRVVVKDLRDDPSAPTIEGMRKAGYPWAMFDENIAPRKT 122
DB 61 EGISEGNTGTSFIVPPEDVPRVVVKDLRDDPSAPTIEGMRKAGYPWAMFDENIAPRKT 120
QY 123 PIQGTGTPDDPKPVILLQLNFIKGGLILTVNGHGAMDMVGQDAVIRLLSKACRNDPFE 182
DB 121 PIQGTGTPDDPKPVILLQLNFIKGGLILTVNGHGAMDMVGQDAVIRLLSKACRNDPFE 180
QY 183 EEMTAMNLDKTIIVPYLNTYIGPEVDHQIVKADVAGDAVLTPVSASWAFPTSPKMS 242
DB 181 EEMTAMNLDKTIIVPYLNTYIGPEVDHQIVKADVAGDAVLTPVSASWAFPTSPKMS 240
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QY 243 ELKDAATKTLDASTKFPVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPAWG 302
DB 241 ELKDAATKTLDASTKFPVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
QY 303 NNPVGLLQNMVTHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLNHNPDKSN 362
DB 301 NNPVGLLQNMVTHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLNHNPDKSN 360
QY 363 VSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFPEVSLMYFMPKPKDGE 422
DB 361 VSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFPEVSLMYFMPKPKDGE 420
QY 423 FCAALSRLDEDMDLKADKEWT 444
DB 421 FCAALSRLDEDMDLKADKEWT 442

RESULT 5
Q9HF40 PRELIMINARY; PRT; 444 AA.
AC Q9HF40;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Trichothecene 3-O-acetyltransferase (Fragment)
OS Gibberella zeae (Fusarium graminearum)
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL28439;
RX MEDLINE=20345085; PubMed=10869425;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910 (2000).
DR EMBL; AF212607; AAG43714.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
DR Transferase.
KW 444
FT NON TER 444 444
SQ SEQUENCE 444 AA; 48625 MW; 317A7085872A8796 CRC64;

Query Match
Best Local Similarity 97.9%; Score 2286; DB 2; Length 444;
Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAFKIQLDITGLQGLLSIYTIQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV 60
DB 1 MAFKIQLDITGLQGLLSIYTIQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV 60
QY 61 KAEGISEGNTGTSFIVPPEDVPRVVVKDLRDDPSAPTIEGMRKAGYPWAMFDENIAPRK 120
DB 61 KAEGISEGNTGTSFIVPPEDVPRVVVKDLRDDPSAPTIEGMRKAGYPWAMFDENIAPRK 120
QY 121 TPIPGTGPDDPKPVILLQLNFIKGGLILTVNGHGAMDMVGQDAVIRLLSKACRNDPF 180
DB 121 TPIPGTGPDDPKPVILLQLNFIKGGLILTVNGHGAMDMVGQDAVIRLLSKACRNDPF 180
QY 181 TEEEMTAMNLDKTIIVPYLNTYIGPEVDHQIVKADVAGDAVLTPVSASWAFPTSPKA 240
DB 181 TEEEMTAMNLDKTIIVPYLNTYIGPEVDHQIVKADVAGDAVLTPVSASWAFPTSPKA 240
QY 241 MSELKDAATKTLDASTKFPVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
DB 241 MSELKDAATKTLDASTKFPVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
QY 301 VSNYPGLLQNMVTHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLNHNPDK 360
DB 301 VSNYPGLLQNMVTHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLNHNPDK 360
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361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420

QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420
Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420

QY 421 GEFCALSLRDEDMRLKADKEWT 444
Db 421 GEFCALSLRDEDMRLKADKEWT 444

RESULT 6
Q9HDF3 PRELIMINARY; PRT; 444 AA.
ID Q9HDF3
AC Q9HDF3
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Trichothecene 3-O-acetyltransferase (Fragment).
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL28721, NRRL28436, NRRL28723, NRRL29010, and NRRL26752;
RX MEDLINE=20345085; PubMed=10869425;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of *Fusarium graminearum*, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910 (2000).
DR EMBL; AF212601; AAG43708.1; -
DR EMBL; AF212582; AAG43689.1; -
DR EMBL; AF212583; AAG43690.1; -
DR EMBL; AF212584; AAG43691.1; -
DR EMBL; AF212594; AAG43701.1; -
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Transferase.
FT NON_TER 444
SQ SEQUENCE 444 AA; 48668 MW; CB8PAP5772696775 CRC64;

Query Match 97.6%; Score 2277; DB 2; Length 444;
Best Local Similarity 99.1%; Pred. No. 4.3e-161;
Matches 440; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 MAFKIQDLTLGQLPGLLSIYQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV 60
Db 1 MAFKIQDLTLGQLPGLLSIYQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV 60
QY 61 KAEGISEGNTGTSFIVPPEDVPRVVVKDLRDDPSAPTEGMRKAGYPWAMFENIIAPRK 120
Db 61 KAEGISEGNTGTSFIVPPEDVPRVVVKDLRDDPSAPTEGMRKAGYPWAMFENIIAPRK 120
QY 121 TLPIGFGTGPDPKPVILLQLNFIKGLLITVNGHGMVGDQDAVIRLLSKACRNDPF 180
Db 121 TLPIGFGTGPDPKPVILLQLNFIKGLLITVNGHGMVGDQDAVIRLLSKACRNDPF 180
QY 181 TEEMTAMNLDKRTIVPYLNTTIGPEVDHQIVKADVAGGDAVLTVPVSASNAFFTFSPKA 240
Db 181 TEEMTAMNLDKRTIVPYLNTTIGPEVDHQIVKADVAGGDAVLTVPVSASNAFFTFSPKA 240
QY 241 MSELKDAATKTLDASTKFSVSTDDALSATFKWSASRVRLERIDGSAPTFCRAVDARPAWG 300
Db 241 MSELKDAATKTLDASTKFSVSTDDALSATFKWSASRVRLERIDGSAPTFCRAVDARPAWG 300
QY 301 VSNYPGLLQNMTHNSTTGEIANESLGATASRLSELDPASMRQTRGLATYLHNNPDK 360
Db 301 VSNYPGLLQNMTHNSTTGEIANESLGATASRLSELDPASMRQTRGLATYLHNNPDK 360
QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420

361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420

QY 421 GEFCALSLRDEDMRLKADKEWT 444
Db 421 GEFCALSLRDEDMRLKADKEWT 444

RESULT 7
Q9HDE8 PRELIMINARY; PRT; 444 AA.
ID Q9HDE8
AC Q9HDE8
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Trichothecene 3-O-acetyltransferase (Fragment).
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL28720, NRRL13818, and NRRL26156;
RX MEDLINE=20345085; PubMed=10869425;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of *Fusarium graminearum*, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910 (2000).
DR EMBL; AF212600; AAG43707.1; -
DR EMBL; AF212597; AAG43704.1; -
DR EMBL; AF212598; AAG43705.1; -
DR EMBL; AF212599; AAG43706.1; -
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Transferase.
FT NON_TER 444
SQ SEQUENCE 444 AA; 48686 MW; DA8314DED9578E7E CRC64;

Query Match 97.5%; Score 2276; DB 2; Length 444;
Best Local Similarity 99.1%; Pred. No. 5.1e-161;
Matches 440; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 MAFKIQDLTLGQLPGLLSIYQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV 60
Db 1 MAFKIQDLTLGQLPGLLSIYQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV 60
QY 61 KAEGISEGNTGTSFIVPPEDVPRVVVKDLRDDPSAPTEGMRKAGYPWAMFENIIAPRK 120
Db 61 KAEGISEGNTGTSFIVPPEDVPRVVVKDLRDDPSAPTEGMRKAGYPWAMFENIIAPRK 120
QY 121 TLPIGFGTGPDPKPVILLQLNFIKGLLITVNGHGMVGDQDAVIRLLSKACRNDPF 180
Db 121 TLPIGFGTGPDPKPVILLQLNFIKGLLITVNGHGMVGDQDAVIRLLSKACRNDPF 180
QY 181 TEEMTAMNLDKRTIVPYLNTTIGPEVDHQIVKADVAGGDAVLTVPVSASNAFFTFSPKA 240
Db 181 TEEMTAMNLDKRTIVPYLNTTIGPEVDHQIVKADVAGGDAVLTVPVSASNAFFTFSPKA 240
QY 241 MSELKDAATKTLDASTKFSVSTDDALSATFKWSASRVRLERIDGSAPTFCRAVDARPAWG 300
Db 241 MSELKDAATKTLDASTKFSVSTDDALSATFKWSASRVRLERIDGSAPTFCRAVDARPAWG 300
QY 301 VSNYPGLLQNMTHNSTTGEIANESLGATASRLSELDPASMRQTRGLATYLHNNPDK 360
Db 301 VSNYPGLLQNMTHNSTTGEIANESLGATASRLSELDPASMRQTRGLATYLHNNPDK 360
QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420
Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420
QY 421 GEFCALSLRDEDMRLKADKEWT 444


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Db      421  GEFCALSLRDEDMDLKADKEWT 444

RESULT 8
Q9HF42
ID      Q9HF42      PRELIMINARY;      PRT;      444  AA.
AC      Q9HF42
DT      01-MAR-2001 (TrEMBLrel. 16, Created)
DT      01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Trichothecene 3-O-acetyltransferase (Fragment).
OS      Gibberella zeae (Fusarium graminearum).
OC      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC      Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX      NCBI_TaxID=5518;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=NRRL26754; PubMed=10869425;
RX      MEDLINE=20345085; PubMed=10869425;
RA      O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT      "Gene genealogies reveal global phylogeographic structure and
RT      reproductive isolation among lineages of Fusarium graminearum, the
RT      fungus causing wheat scab.";
RL      Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910(2000).
DR      ENBL; AP212595; AAG43702.1; -.
DR      GO; GO:0016740; F:transferase activity; IEA.
DR      InterPro; IPR003480; Transferase.
DR      Pfam; PF02458; Transferase; 1.
KW      Transferase.
FT      NON TER      444      444
SQ      SEQUENCE      444  AA; 48682 MW; 242895FE652F3E16 CRC64;

Query Match      97.5%; Score 2276; DB 2; Length 444;
Best Local Similarity 98.9%; Pred. No. 5.1e-161;
Matches 439; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1  MAFKIQDLTGLQPLGLLSIYQISLLYPVSDSQYPTIVSTFQGLKRSEAVPWAGQV 60
DB      1  MAFKIQDLTGLQPLGLLSIYQISLLYPVSDSQYPTIVSTFQGLKRSEAVPWAGQV 60
QY      61  KAEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTEIEGMKAGYPMAMFDENIIAPRK 120
DB      61  KAEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTEIEGMKAGYPMAMFDENIIAPRK 120
QY      121  TLPFGTGPDDPKPVILLQLNFIKGLILTVNGQHGAMDMVQGDVAVIRLLSKACRNDPF 180
DB      121  TLPFGTGPDDPKPVILLQLNFIKGLILTVNGQHGAMDMVQGDVAVIRLLSKACRNDPF 180
QY      181  TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGGDVLTVPVSASWAFFTSPKA 240
DB      181  TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGGDVLTVPVSASWAFFTSPKA 240
QY      241  MSELKDAATKTLDASTKFTVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPMG 300
DB      241  MSELKDAATKTLDASTKFTVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPMG 300
QY      301  VSNYPGLLQNMITYHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLHNNPK 360
DB      301  VSNYPGLLQNMITYHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLHNNPK 360
QY      361  SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGPKETVRRPIFPVPSLAMYFMPKKPD 420
DB      361  SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGPKETVRRPIFPVPSLAMYFMPKKPD 420
QY      421  GEFCALSLRDEDMDLKADKEWT 444
DB      421  GEFCALSLRDEDMDLKADKEWT 444

RESULT 9
Q9HF41
ID      Q9HF41      PRELIMINARY;      PRT;      444  AA.
AC      Q9HF41
DT      01-MAR-2001 (TrEMBLrel. 16, Created)
DT      01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Trichothecene 3-O-acetyltransferase (Fragment).
OS      Gibberella zeae (Fusarium graminearum).
OC      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC      Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX      NCBI_TaxID=5518;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=NRRL26754; PubMed=10869425;
RX      MEDLINE=20345085; PubMed=10869425;
RA      O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT      "Gene genealogies reveal global phylogeographic structure and
RT      reproductive isolation among lineages of Fusarium graminearum, the
RT      fungus causing wheat scab.";
RL      Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910(2000).
DR      ENBL; AP212595; AAG43702.1; -.
DR      GO; GO:0016740; F:transferase activity; IEA.
DR      InterPro; IPR003480; Transferase.
DR      Pfam; PF02458; Transferase; 1.
KW      Transferase.
FT      NON TER      444      444
SQ      SEQUENCE      444  AA; 48682 MW; 242895FE652F3E16 CRC64;

Query Match      97.5%; Score 2276; DB 2; Length 444;
Best Local Similarity 98.9%; Pred. No. 5.1e-161;
Matches 439; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1  MAFKIQDLTGLQPLGLLSIYQISLLYPVSDSQYPTIVSTFQGLKRSEAVPWAGQV 60
DB      1  MAFKIQDLTGLQPLGLLSIYQISLLYPVSDSQYPTIVSTFQGLKRSEAVPWAGQV 60
QY      61  KAEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTEIEGMKAGYPMAMFDENIIAPRK 120
DB      61  KAEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTEIEGMKAGYPMAMFDENIIAPRK 120
QY      121  TLPFGTGPDDPKPVILLQLNFIKGLILTVNGQHGAMDMVQGDVAVIRLLSKACRNDPF 180
DB      121  TLPFGTGPDDPKPVILLQLNFIKGLILTVNGQHGAMDMVQGDVAVIRLLSKACRNDPF 180
QY      181  TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGGDVLTVPVSASWAFFTSPKA 240
DB      181  TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGGDVLTVPVSASWAFFTSPKA 240
QY      241  MSELKDAATKTLDASTKFTVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPMG 300
DB      241  MSELKDAATKTLDASTKFTVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPMG 300
QY      301  VSNYPGLLQNMITYHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLHNNPK 360
DB      301  VSNYPGLLQNMITYHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLHNNPK 360
QY      361  SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGPKETVRRPIFPVPSLAMYFMPKKPD 420
DB      361  SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGPKETVRRPIFPVPSLAMYFMPKKPD 420
QY      421  GEFCALSLRDEDMDLKADKEWT 444
DB      421  GEFCALSLRDEDMDLKADKEWT 444

RESULT 10
Q9HDN2
ID      Q9HDN2      PRELIMINARY;      PRT;      444  AA.
AC      Q9HDN2
DT      01-MAR-2001 (TrEMBLrel. 16, Created)
DT      01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Trichothecene 3-O-acetyltransferase (Fragment).
OS      Gibberella zeae (Fusarium graminearum).
OC      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC      Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX      NCBI_TaxID=5518;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=NRRL26754; PubMed=10869425;
RX      MEDLINE=20345085; PubMed=10869425;
RA      O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT      "Gene genealogies reveal global phylogeographic structure and
RT      reproductive isolation among lineages of Fusarium graminearum, the
RT      fungus causing wheat scab.";
RL      Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910(2000).
DR      ENBL; AP212595; AAG43702.1; -.
DR      GO; GO:0016740; F:transferase activity; IEA.
DR      InterPro; IPR003480; Transferase.
DR      Pfam; PF02458; Transferase; 1.
KW      Transferase.
FT      NON TER      444      444
SQ      SEQUENCE      444  AA; 48698 MW; 727582A1EAA15518 CRC64;

Query Match      97.4%; Score 2273; DB 2; Length 444;
Best Local Similarity 98.9%; Pred. No. 8.5e-161;
Matches 439; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1  MAFKIQDLTGLQPLGLLSIYQISLLYPVSDSQYPTIVSTFQGLKRSEAVPWAGQV 60
DB      1  MAFKIQDLTGLQPLGLLSIYQISLLYPVSDSQYPTIVSTFQGLKRSEAVPWAGQV 60
QY      61  KAEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTEIEGMKAGYPMAMFDENIIAPRK 120
DB      61  KAEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTEIEGMKAGYPMAMFDENIIAPRK 120
QY      121  TLPFGTGPDDPKPVILLQLNFIKGLILTVNGQHGAMDMVQGDVAVIRLLSKACRNDPF 180
DB      121  TLPFGTGPDDPKPVILLQLNFIKGLILTVNGQHGAMDMVQGDVAVIRLLSKACRNDPF 180
QY      181  TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGGDVLTVPVSASWAFFTSPKA 240
DB      181  TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGGDVLTVPVSASWAFFTSPKA 240
QY      241  MSELKDAATKTLDASTKFTVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPMG 300
DB      241  MSELKDAATKTLDASTKFTVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPMG 300
QY      301  VSNYPGLLQNMITYHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLHNNPK 360
DB      301  VSNYPGLLQNMITYHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLHNNPK 360
QY      361  SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGPKETVRRPIFPVPSLAMYFMPKKPD 420
DB      361  SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGPKETVRRPIFPVPSLAMYFMPKKPD 420
QY      421  GEFCALSLRDEDMDLKADKEWT 444
DB      421  GEFCALSLRDEDMDLKADKEWT 444

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OX NCBI_TaxID=5518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL28718, NRRL2903, and NRRL28585;
RA MEDLINE=20345085; PubMed=10869425;
RX O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910 (2000).
DR EMBL; AF212587; AAG43694.1; -.
DR EMBL; AF212585; AAG43692.1; -.
DR EMBL; AF212586; AAG43693.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Transferase.
FT NON TER 444
SQ SEQUENCE 444 AA; 48638 MW; 12A8337C5320COAD CRC64;

Query Match 97.3%; Score 2272; DB 2; Length 444;
Best Local Similarity 98.9%; Pred. No. 1e-160;
Matches 439; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAFKIQDLTGLQPLGLLSIYTIQISLLYPVSDSSQYPTIVSTFEOGLKRFSEAVPWVAGQV 60
Db 1 MAFKIQDLTGLQPLGLLSIYTIQISLLYPVSDPSQYPAIVSTFEOGLKRFSEAVPWVAGQV 60
QY 61 KAEGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAFMFENIIAPRK 120
Db 61 KAEGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAFMFENIIAPRK 120
QY 121 TLPIGCTGPDPPKPVILLQLNFIKGLLITVNGHGMVMQDQDAVIRLLSKACRNDPF 180
Db 121 TLPIGCTGPDPPKPVILLQLNFIKGLLITVNGHGMVMQDQDAVIRLLSKACRNDPF 180
QY 181 TEEMTAMNLDRTIIVPYLNTYIGPEVDHQIVKPDVAGGDAVLTVPVSASWAFFTSPKA 240
Db 181 TEEMTAMNLDRTIIVPYLNTYIGPEVDHQIVKPDVAGGDAVLTVPVSASWAFFTSPKA 240
QY 241 MSELKDAATKTLDASTKFDVSTDDALSAPFWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
Db 241 MSELKDAATKTLDASTKFDVSTDDALSAPFWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
QY 301 VSNYPGLLQNMVTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLHNNPK 360
Db 301 VSNYPGLLQNMVTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLHNNPK 360
QY 361 SNVSLTADADPSTVMSLSSWAKVGLWDYDFGLGKGPETVRRPIFEPVSLMYFMPKKPD 420
Db 361 SNVSLTADADPSTVMSLSSWAKVGLWDYDFGLGKGPETVRRPIFEPVSLMYFMPKKPD 420
QY 421 GFCAALSURDEDMRLKADKEWT 444
Db 421 GFCAALSURDEDMRLKADKEWT 444

RESULT 11
Q9HD15 PRELIMINARY; PRT; 444 AA.
AC Q9HD15;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Trichothecene 3-O-acetyltransferase (Fragment).
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Nectriales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL29148, and NRRL25797;
RX MEDLINE=20345085; PubMed=10869425;

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RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910 (2000).
DR EMBL; AF212589; AAG43696.1; -.
DR EMBL; AF212588; AAG43695.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Transferase.
FT NON TER 444
SQ SEQUENCE 444 AA; 48680 MW; 69A6A48E702227C3 CRC64;

Query Match 97.3%; Score 2271; DB 2; Length 444;
Best Local Similarity 98.9%; Pred. No. 1.2e-160;
Matches 439; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAFKIQDLTGLQPLGLLSIYTIQISLLYPVSDSSQYPTIVSTFEOGLKRFSEAVPWVAGQV 60
Db 1 MAFKIQDLTGLQPLGLLSIYTIQISLLYPVSDPSQYPTIVSTFEOGLKRFSEAVPWVAGQV 60
QY 61 KAEGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAFMFENIIAPRK 120
Db 61 KAEGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAFMFENIIAPRK 120
QY 121 TLPIGCTGPDPPKPVILLQLNFIKGLLITVNGHGMVMQDQDAVIRLLSKACRNDPF 180
Db 121 TLPIGCTGPDPPKPVILLQLNFIKGLLITVNGHGMVMQDQDAVIRLLSKACRNDPF 180
QY 181 TEEMTAMNLDRTIIVPYLNTYIGPEVDHQIVKPDVAGGDAVLTVPVSASWAFFTSPKA 240
Db 181 TEEMTAMNLDRTIIVPYLNTYIGPEVDHQIVKPDVAGGDAVLTVPVSASWAFFTSPKA 240
QY 241 MSELKDAATKTLDASTKFDVSTDDALSAPFWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
Db 241 MSELKDAATKTLDASTKFDVSTDDALSAPFWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
QY 301 VSNYPGLLQNMVTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLHNNPK 360
Db 301 VSNYPGLLQNMVTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLHNNPK 360
QY 361 SNVSLTADADPSTVMSLSSWAKVGLWDYDFGLGKGPETVRRPIFEPVSLMYFMPKKPD 420
Db 361 SNVSLTADADPSTVMSLSSWAKVGLWDYDFGLGKGPETVRRPIFEPVSLMYFMPKKPD 420
QY 421 GFCAALSURDEDMRLKADKEWT 444
Db 421 GFCAALSURDEDMRLKADKEWT 444

RESULT 12
Q9HDE0 PRELIMINARY; PRT; 444 AA.
AC Q9HDE0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Trichothecene 3-O-acetyltransferase (Fragment).
OS Fusarium cerealis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=56641;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL25805, and NRRL25491;
RX MEDLINE=20345085; PubMed=10869425;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910 (2000).
DR EMBL; AF212613; AAG43720.1; -.

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Query Match	96.7%	Score 2257;	DB 2;	Length 444;
Best Local Similarity	98.0%;	Pred. No. 1.3e-159;		
Matches 435; Conservative	4;	Mismatches 5;	Indels 0;	Gaps 0;

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QY 1 MAFKIQLDTLGLPGLLSIYTOISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV 60
DB 1 MAFKIQLDTLGLPGLLSIYTOISLLYPVSDPSQYPTIVSTFEQGLKRFSEAVPWVAGQV 60
QY 61 KAEGISEGNTGTSFIVPFEDVRVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRK 120
DB 61 KAEGISEGNTGTSFIVPFEDVRVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRK 120
QY 121 TLPFGTGPDPKPVILLQNLFIKGLLITVNGHGMVQDVAIRLLSKACRNDPF 180
DB 121 TLPFGTGPDPKPVILLQNLFIKGLLITVNGHGMVQDVAIRLLSKACRNDPF 180
QY 181 TEEEMTAMNLDKRTIVPYLENYTTIGPEVDHQIVKADVAGGDAVLTVPVSASWAFTFSPKA 240
DB 181 TEEEMTAMNLDKRTIVPYLENYTTIGPEVDHQIVKADVAGGDAVLTVPVSASWAFTFSPKA 240
QY 241 MSELKDAATKTLDASTKFKVSTDDALSFAFWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
DB 241 MSELKDAATKTLDASTKFKVSTDDALSFAFWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
QY 301 VSNYPGLLQNNYTHNSTIGEIANESLGATASRLRSELDPASMRQTRGLATYILHNNPDK 360
DB 301 VSNYPGLLQNNYTHNSTIGEIANESLGATASRLRSELDPASMRQTRGLATYILHNNPDK 360
QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKPKPD 420
DB 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKPKPD 420
QY 421 GEFCAALSRLRDEDMDLKADKEWT 444
DB 421 GEFCAALSRLRDEDMDLKADKEWT 444

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RESULT 15

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Q9HF39 ID Q9HF39 PRELIMINARY; PRT; 444 AA.
AC Q9HF39;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Trichothecene 3-O-acetyltransferase (fragment).
OS Fusarium cerealis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=56641;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=NRRL3721;
RX MEDLINE=20345085; PubMed=10869425;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab."
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910 (2000).
DR EMBL; AF212611; AAC43718.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; transferase.
DR Pfam; PF02459; Transferase; 1.
KW Transferase.
FT NON TER 444 444
SQ SEQUENCE 444 AA; 48694 MW; FCA1047B43207194 CRC64;

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Query Match 96.6%; Score 2255; DB 2; Length 444;
 Best Local Similarity 98.0%; Pred. No. 1.9e-159;
 Matches 435; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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QY 1 MAFKIQLDTLGLPGLLSIYTOISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV 60
DB 1 MAFKIQLDTLGLPGLLSIYTOISLLYPVSDPSQYPTIVSTFEQGLKRFSEAVPWVAGQV 60
QY 61 KAEGISEGNTGTSFIVPFEDVRVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRK 120

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DB 61 KAEGISEGNTGTSFIVPFEDVRVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRK 120
QY 121 TLPFGTGPDPKPVILLQNLFIKGLLITVNGHGMVQDVAIRLLSKACRNDPF 180
DB 121 TLPFGTGPDPKPVILLQNLFIKGLLITVNGHGMVQDVAIRLLSKACRNDPF 180
QY 181 TEEEMTAMNLDKRTIVPYLENYTTIGPEVDHQIVKADVAGGDAVLTVPVSASWAFTFSPKA 240
DB 181 TEEEMTAMNLDKRTIVPYLENYTTIGPEVDHQIVKADVAGGDAVLTVPVSASWAFTFSPKA 240
QY 241 MSELKDAATKTLDASTKFKVSTDDALSFAFWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
DB 241 MSELKDAATKTLDASTKFKVSTDDALSFAFWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
QY 301 VSNYPGLLQNNYTHNSTIGEIANESLGATASRLRSELDPASMRQTRGLATYILHNNPDK 360
DB 301 VSNYPGLLQNNYTHNSTIGEIANESLGATASRLRSELDPASMRQTRGLATYILHNNPDK 360
QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKPKPD 420
DB 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKPKPD 420
QY 421 GEFCAALSRLRDEDMDLKADKEWT 444
DB 421 GEFCAALSRLRDEDMDLKADKEWT 444

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Search completed: January 23, 2005, 19:49:07
 Job time : 113 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2005, 19:32:07 ; Search time 32 Seconds
(without alignments)
934.669 Million cell updates/sec

Title: US-10-614-954-6
Perfect score: 2334
Sequence: 1 MAFKIQDLTGLQLPGLLSIY.....EDMDRLKADKEWKYQAYVG 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents AA:*
- 1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
 - 2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
 - 3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
 - 4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
 - 5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
 - 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2334	100.0	451	3	US-09-538-414-6
2	2334	100.0	451	4	US-10-074-279-6
3	1860.5	79.7	459	3	US-09-538-414-2
4	1860.5	79.7	459	4	US-10-074-279-2
5	962.5	41.2	474	3	US-09-538-414-8
6	962.5	41.2	474	4	US-10-074-279-8
7	142	6.1	448	3	US-09-457-046B-56
8	141.5	6.1	436	3	US-09-457-046B-62
9	134	5.7	448	1	US-08-207-904-2
10	134	5.7	448	1	US-08-207-904-17
11	132	5.6	439	3	US-09-457-046B-28
12	130.5	5.6	451	3	US-09-457-046B-69
13	126.5	5.4	435	3	US-09-457-046B-60
14	125.5	5.4	439	3	US-09-457-046B-68
15	124	5.3	445	3	US-09-457-046B-73
16	122	5.2	433	3	US-09-457-046B-66
17	121.5	5.2	306	3	US-09-457-046B-22
18	121.5	5.2	482	3	US-09-457-046B-63
19	118	5.1	450	3	US-09-457-046B-67
20	117	5.0	830	4	US-09-562-737-34
21	113	4.8	440	3	US-09-457-046B-45
22	112	4.8	441	3	US-09-457-046B-54
23	110.5	4.7	1858	4	US-09-489-039A-11380
24	106.5	4.6	303	3	US-09-457-046B-20
25	105.5	4.5	446	3	US-09-457-046B-74
26	105.5	4.5	3724	2	US-08-804-227C-10
27	105.5	4.5	3724	2	US-08-804-198-4

28	104.5	4.5	769	4	US-09-248-796A-18265	Sequence 18265, A
29	104.5	4.5	1337	3	US-08-854-585-2	Sequence 2, Appli
30	104.5	4.5	1337	4	US-09-447-533-2	Sequence 2, Appli
31	104.5	4.5	1337	5	PCT-US95-05512-2	Sequence 2, Appli
32	104	4.5	302	3	US-09-457-046B-24	Sequence 24, Appli
33	103.5	4.4	458	3	US-09-457-046B-61	Sequence 61, Appli
34	102.5	4.4	810	4	US-09-583-110-4352	Sequence 4352, Ap
35	102	4.4	802	3	US-09-147-236-4	Sequence 4, Appli
36	102	4.4	802	4	US-09-522-474-4	Sequence 4, Appli
37	100	4.3	461	3	US-09-457-046B-70	Sequence 70, Appli
38	99.5	4.3	455	3	US-09-457-046B-72	Sequence 72, Appli
39	99.5	4.3	1289	2	US-08-542-003-2	Sequence 2, Appli
40	99.5	4.3	1289	2	US-08-322-760A-2	Sequence 2, Appli
41	99.5	4.3	1289	4	US-09-236-949-2	Sequence 2, Appli
42	99	4.2	306	3	US-09-457-046B-2	Sequence 2, Appli
43	98.5	4.2	560	2	US-08-981-690-2	Sequence 2, Appli
44	98.5	4.2	610	4	US-09-455-777-2	Sequence 2, Appli
45	97	4.2	347	4	US-09-328-352-7107	Sequence 7107, Ap

ALIGNMENTS

RESULT 1
US-09-538-414-6
; Sequence 6, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Fusarium graminearum
US-09-538-414-6

Query Match	100.0%	Score 2334;	DB 3;	Length 451;
Best Local Similarity	100.0%;	Pred. No. 1.1e-233;		
Matches 451;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MAFKIQDLTGLQLPGLLSIYTOISLLYPVSDSQYPTIVSTFQGLKRFSEAVPWAGQV	60	
DB	1	MAFKIQDLTGLQLPGLLSIYTOISLLYPVSDSQYPTIVSTFQGLKRFSEAVPWAGQV	60	
QY	61	KAEIGSEGNSTGTSFIVPFEDVPRVVVKLDLDDPSAPTIEGMRKAGYPMAMFENIAPRK	120	
DB	61	KAEIGSEGNSTGTSFIVPFEDVPRVVVKLDLDDPSAPTIEGMRKAGYPMAMFENIAPRK	120	
QY	121	TLPIGPGTGPDDPKPVILLQLNFIKGLLITVNGQHGAMDVGQDAVIRLLSKACRNDPF	180	
DB	121	TLPIGPGTGPDDPKPVILLQLNFIKGLLITVNGQHGAMDVGQDAVIRLLSKACRNDPF	180	
QY	181	TEEMTAMNLDKRTIIVPYLNTYTGPEVDHQIKVADVAGDVAVLTPVSASWAFFTSPKA	240	
DB	181	TEEMTAMNLDKRTIIVPYLNTYTGPEVDHQIKVADVAGDVAVLTPVSASWAFFTSPKA	240	
QY	241	MSELKDAATKTLDASTKVFSTDDALSAFIWKSASRVRLERIDGSAPTFCRAVDAPAMG	300	
DB	241	MSELKDAATKTLDASTKVFSTDDALSAFIWKSASRVRLERIDGSAPTFCRAVDAPAMG	300	
QY	301	VSNYPGLLQNTYHNTSTTGTEIANESIGATASRLSELDPASRQRTGLATYLHNHPDK	360	

Db 301 VSNYPGLLQNMVTHNSTTGEIANESLGATASRLRSELDPASMRQRTGLATYLNHNPKD 360
Qy 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVTRRPIPEPVESLMVFMKPKPD 420
Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVTRRPIPEPVESLMVFMKPKPD 420
Qy 421 GEFCALSLRDEDMRLKADKWKTKYQYVG 451
Db 421 GEFCALSLRDEDMRLKADKWKTKYQYVG 451

RESULT 2
US-10-074-279-6
; Sequence 6, Application US/10074279
; Patent No. 6646184
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Fusarium graminearum
US-10-074-279-6

Query Match 100.0%; Score 2334; DB 4; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.1e-233;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAFKIQDLTGQPLGLSIYTOISLVPVSDSSQYPTIVSTFPGQIKRFSEAVPWVAGQV 60
Db 1 MAFKIQDLTGQPLGLSIYTOISLVPVSDSSQYPTIVSTFPGQIKRFSEAVPWVAGQV 60
Qy 61 KAEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTEIGMRKAGYPMAMFDENIAPRK 120
Db 61 KAEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTEIGMRKAGYPMAMFDENIAPRK 120
Qy 121 TLPIGPGTGDDPKPVILLQNLNFIKGGILITVNGQHGMDMVGDQDAVIRLLSKACRNDPF 180
Db 121 TLPIGPGTGDDPKPVILLQNLNFIKGGILITVNGQHGMDMVGDQDAVIRLLSKACRNDPF 180
Qy 181 TEEMTAMNLDRTKIIVPYLENTYIGPEVDHQIVKADVAGGDVLTVPVSASWAFPTSPKA 240
Db 181 TEEMTAMNLDRTKIIVPYLENTYIGPEVDHQIVKADVAGGDVLTVPVSASWAFPTSPKA 240
Qy 241 MSELKDAATKTLDASTKFSVTDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPMG 300
Db 241 MSELKDAATKTLDASTKFSVTDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPMG 300
Qy 301 VSNYPGLLQNMVTHNSTTGEIANESLGATASRLRSELDPASMRQRTGLATYLNHNPKD 360
Db 301 VSNYPGLLQNMVTHNSTTGEIANESLGATASRLRSELDPASMRQRTGLATYLNHNPKD 360
Qy 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVTRRPIPEPVESLMVFMKPKPD 420
Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVTRRPIPEPVESLMVFMKPKPD 420
Qy 421 GEFCALSLRDEDMRLKADKWKTKYQYVG 451
Db 421 GEFCALSLRDEDMRLKADKWKTKYQYVG 451

RESULT 3
US-09-538-414-2
; Sequence 2, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Fusarium sporotrichioides
US-09-538-414-2

Query Match 79.7%; Score 1860.5; DB 3; Length 459;
Best Local Similarity 77.6%; Pred. No. 2e-184;
Matches 349; Conservative 50; Mismatches 50; Indels 1; Gaps 1;
Qy 2 AFKIQDLTGQPLGLSIYTOISLVPVSDSSQYPTIVSTFPGQIKRFSEAVPWVAGQV 61
Db 11 SFDIELDIIOQOPLLSIYTOISLVPVSDSPSYPTIVSTLEEGKRLJSQTFPWVAGQV 70
Qy 62 AEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTEIGMRKAGYPMAMFDENIAPRK 121
Db 71 TEGISEGNTGTSKIIPYEETPLVVKDLRDDSSAPTEIGLRKAGFLEMFENNVAPRK 130
Qy 122 LPIGPGTGDDPKPVILLQNLNFIKGGILITVNGQHGMDMVGDQDAVIRLLSKACRNDPF 181
Db 131 LAIGPENGNDPKPVILLQNLNFIKGGILITVNGQHGMDMTGQDAIIRLLSKACRNEST 190
Qy 182 EEMTAMNLDRTKIIVPYLENTYIGPEVDHQIVKADVAGGDVLTVPVSASWAFPTSPKA 241
Db 191 EBEISAMNLDRTKIIVPYLENTYIGPEVDHQIADKAPA-GDAPPAKASWAFPTSPKAL 249
Qy 242 SELKDAATKTLDASTKFSVTDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPMGV 301
Db 250 SELKDAATKTLDASTKFSVTDALSAFIWQSTSRVRLARLDASTPTTEFCRAVDMRGPVG 309
Qy 302 SNYPGLLQNMVTHNSTTGEIANESLGATASRLRSELDPASMRQRTGLATYLNHNPKDS 361
Db 310 SSTYPCLLQNMVTHDSTVAEIANEPLGATASRLRSELNDRRLRRRTQALATYMHGLPDKS 369
Qy 362 NVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVTRRPIPEPVESLMVFMKPKPDG 421
Db 370 VSVSLTADANPSSIMLSSWAKVGCWEYDFGGLGKPEVTRRPFEPFESLMVFMKPKPDG 429
Qy 422 EFCAALSLRDEDMRLKADKWKTKYQYVG 451
Db 430 EFTASISLRDEDMERLKADDEWTKYKYIG 459

RESULT 4
US-10-074-279-2
; Sequence 2, Application US/10074279
; Patent No. 6646184
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.

```

; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Fusarium sporotrichioides
US-10-074-279-2

Query Match      79.7%; Score 1860.5; DB 4; Length 459;
Best Local Similarity 77.6%; Pred. No. 2e-184;
Matches 349; Conservative 50; Mismatches 50; Indels 1; Gaps 1;

QY 2 AFKIQDITGQLPGLLSIYTOISLLYPVSDSSQYPTIVSTFEOGLKRFSEAVPWVAGQVK 61
Db 11 SPDIELDIQQPPLLSIYTOISLVYPVSDPSQYPTIVSTLEGLKRLSQTFPWVAGQVK 70
QY 62 AEGISEGNTGTSFIYVPFEDVPRVVKDLRDDSPAPTIEGMRKAGYPMAMFENIAPRKT 121
Db 71 TEGISEGNTGTSKIPIYEETPRLVKDLRDDSSAPTIEGLRKAGPPEMFEDENVAPRKT 130
QY 122 LPIGPGTGPDDPKPVILLQNLFIKGLILTVNGQHGMDVMGQDAVIRLLSKACRNDPPT 181
Db 131 LAIGFONGFNDPKPVULLQNLFIKGLILTVNGQHGMDMTQDAIIRLLSKACRNEST 190
QY 182 EBEEMTNLDRTKIYVPLENYTIGPEVDHQIVKADVAGGDAVLTVPVSAWAPFTFSPKAM 241
Db 191 EBEISAMNLDRTKIVPLENYKVGPPELDHQIAKPAPA-GDAPPAPAKASWAFESFTPKAL 249
QY 242 SELKDAATKTLDASTKFSVSTDALSFAIWKASRVLEIRIDGSAPTEFCRAVDARPAMGV 301
Db 250 SELKDAATKTLDASSKFSVSTDALSFAIWQSTSRVLAELDASTPTEFCRAVDMRGPMSGV 309
QY 302 SNYPGGLQNMTYHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLNHPDKS 361
Db 310 SSTYPGGLQNMTYHDSVTAEIANEPICATASRLRSELNDRIRRTQALATYHGLPDKS 369
QY 362 NVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLAMYFMPKCKPDG 421
Db 370 SVSLTADANPSSIMLSSWAKVGCWEYDFGLGKGPESVRRPRFEPFESLAMYFMPKCKPDG 429
QY 422 EFCALSLRDEMDRLKADKEWTKYAYVG 451
Db 430 EFTASISLRDEMERLKADEEWTYKAYIG 459

RESULT 5
US-09-538-414-8
; Sequence 8, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-074-279-8

Query Match      41.2%; Score 962.5; DB 4; Length 474;
Best Local Similarity 44.4%; Pred. No. 4.9e-91;
Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;

QY 6 QLDITGQLPGLLSIYTOISLLYPVSDSSQYPTIVSTFEOGLKRFSEAVPWVAGQVKAEGI 65
Db 22 QLDILGQPPSLYKLYTQICSIYRVPDPSAHDHIVNTLTRGLTAKNFQWLGNVVEGA 81
QY 66 SEGNTGTSFIYVPFEDVPRVVKDLRDDSPAPTIEGMRKAGYPMAMFENIAPRKT-PI 124
Db 82 DEGNTGTYRIVPESDKIP-LIIVQDLREDLSAPTMSLEKADFFIYMLDEKTFAPCMTINPP 140
QY 125 GPGTG-PDDPKPVIILLQNLFIKGLILTVNGQHGMDVMGQDAVIRLLSKACRNDPFTBE 183
Db 141 GNTIGMAAKSGPFAVQANFISGGLVLTIVGQHNIMDITQGESIINLLANKSCHQKFFSDE 200
QY 184 ENTAMNLDRTKIYVPLENYTIGPEVD--HQIVKA--DVAGGDAVLTVPV--ASWAPFTFSP 238
Db 201 ELLIGNIDKSKSIPLFDE--TWEPTDTTLVHEIVETSRNTSGEEKEQSCSSNTWAYVEFSA 259
QY 239 KAMSELKDAATKTLDASTKFSVSTDALSFAIWKASRVLEIRIDGSAPTEFCRAVDARPA 298
Db 260 ISLQNLIRILAMOTCTSGTKFVSTDDIVTAFIWKSVSRARLSRLKPKETKSNLGRAVDVRKR 319
QY 299 MGVSNNYPGGLQNMTYHNSTIGEIANESLGATASRLRSELDP--SMRQRTGLATYLNH 356
Db 320 LGLPETYGGLLVNMTFNTGSLKSLDHSKLSGLVSLASQIRRLKDPKVPDLAYNTCALATLSR 379
QY 357 NPKDSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLAMYFMP 416
Db 380 CPDKTKVSIQPIDTLTSGIMVSSWAKVSLYDVFDFNLGLGKPKSVRRPRFISLESIIYFMP 439
QY 417 KXPDEGFCALSLRDEMDRLKADKEWTKYAYVG 451
Db 440 RSSRGMVVALCLRDKWECLNADKEWTNYATHIG 474

RESULT 6
US-10-074-279-8
; Sequence 8, Application US/10074279
; Patent No. 6646184
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-074-279-8

Query Match      41.2%; Score 962.5; DB 4; Length 474;
Best Local Similarity 44.4%; Pred. No. 4.9e-91;
Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;

QY 6 QLDITGQLPGLLSIYTOISLLYPVSDSSQYPTIVSTFEOGLKRFSEAVPWVAGQVKAEGI 65
Db 22 QLDILGQPPSLYKLYTQICSIYRVPDPSAHDHIVNTLTRGLTAKNFQWLGNVVEGA 81
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QY 66 SEGNTGTSFIVFEDVPRVVKDLRDDPSAPTIEGRKAGVPMAMFENIAPRKL-PI 124
DB 82 DEGNTGTVRIVPSDKIP-LIVQDLREDUSAPTMSLEKADFFIYMLDKTAPACMTINPP 140
QY 125 GPGTG-PDDPKVILLQNLFIKGGILTVNGQHGAMDMVGDVAVIRLLSKACRNDPFTTE 183
DB 141 GNTIGMAKSGFVAVQANFISGLGLVITVQHNIMDITQBSIINLLNKSCHQKPFSD 200
QY 184 ENTAMNLDKRTTVPLENTYIGPEVD--HOIYKA--DVAGGDVAVITPVS-ASWAFPTSP 238
DB 201 ELLIGNIDKSGIPLFDE-TWEPDITLVEHIVETSRTSGEKEQSCSSNSTWAYFEFSA 259
QY 239 KAMSELKDAATKTLDASTKFTVSTDDALSFAIWKASRVRLERIDGSAFTEFCRAVDARPA 298
DB 260 ISLQNLRIILAMOTCTGTFKFTVSTDDIVTAFIWKSVSRARLSRLKETKSNLGRVAVDKR 319
QY 299 MGVSNNYPGLLQNMVTHNSTIGEIANESLGATASRLSELDP--SMRQRTGLATYILHN 356
DB 320 LGLPETYPGLLVNMTFTGSLKSLDKSLGVLASQIRRLKDPKVPDLAYNTCALATLLSR 379
QY 357 NPDKNVSUTADADPSTSVMLSSWAKVGLWDYDFGLGCKPFTVRPIPEPVSLEMYMP 416
DB 380 CPDKTKVSIPOPTDITLSGIMVSWAKVSLYDVFNLGLGKPKSVRRPRFISLESIIYMP 439
QY 417 KXPDPGEFCAALSIRDEDMRLKADKWTYKVAOVVG 451
DB 440 RSRGEMVVALCLURDKWELCLNADKWTNYATHIG 474

RESULT 7
US-09-457-046B-56
; Sequence 56, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 56
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-09-457-046B-56

Query Match 6.1%; Score 142; DB 3; Length 448;
Best Local Similarity 20.5%; Pred. No. 9.2e-06;
Matches 84; Conservative 61; Mismatches 184; Indels 80; Gaps 16;

QY 5 IQDITGQLPGLLSIYQISLLYPVSDSSQYPIVSTFEOGLKRFSEAVPWVAGOVKAEG 64
DB 35 LQLSAVDRLPFGMKFATFSVAVLVNASSHSIFANPAQIIQALSKEVIQYYPAPAGRIRQKE 94
QY 65 ISB-----GNTGTSFIVFEDVPRVVKDLRDDPSAPTIEGRKAGVPMAMFENIAPR 119
DB 95 NEELEVECTEGALFVAVLVNDLSVLRLD-----DAQNASYEQLLF----- 136
QY 120 KTLPIGPGTGDDPKPVILLQNLFIKGGILTVNGQHGAMDMVGDVAVIRLLSKACRND- 178
DB 137 -SLP--ENIQVQDLHLPLILQVTRFTCGFVGVGVGFHIGICDARGGTQFLQGLADMARGET 193
QY 179 -PFTTEEWAMNLDKRTIVP-----YLENTYIGPEVDHOIYKADVAGGDVAVITPVSASWAF 233
DB 194 KPLVEPVW-----NRELKPEDLMHLQFHKFG--LIRQPLKLD-----EICOAS 235
QY 234 FTFGPKAMSELKDAATKTLDASTKFTVSTDDALSFAIWKASRVRLERIDGSAFTEFCRAV 293
DB 236 FTINSEILNIYKQC---VIEECNEIFSAFVWVWALTW--IARTKAFQIPHNNVMMFLGM 290
QY 294 DARPAMGVSNYPGLLQNMVTHNSTIG-----EIANESLGATASRLSELDPASMR 344

DB 291 DARYFN-----PPLPKG--YYGNAICTSCVNIENVQDLLNGSLSRAMWITKSKIPLIEN 343
QY 345 QRTGLATYILHNNDKGNVSLTADADPSTSVMLSSWAKVGLWDYDFGLG 393
DB 344 LRSRIVA-----NQSGVD--EIKHENVVVFGDWRRLGFHEYDFGSG 383

RESULT 8
US-09-457-046B-62
; Sequence 62, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 62
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-62

Query Match 6.1%; Score 141.5; DB 3; Length 436;
Best Local Similarity 22.2%; Pred. No. 9.9e-06;
Matches 74; Conservative 56; Mismatches 133; Indels 71; Gaps 14;

QY 135 PVILLQNLFIK--GGILTVNGQHGAMDMVGDVAVIRLLSKACRN-----DPFTE----- 182
DB 135 PVLLIQANFFSCGGLVITICVSHKITDATSLAMIRGWAESSRGLGITLIFSFTASEVFP 194
QY 183 ---EEMTAMNLDKRTIVPYLENTYIGPEVDHOIYKADVAGGDVAVITPVSASWAFPTSPK 239
DB 195 KPLDLPSKPMDRK-----EEVEE-----MSCVTGRFVFDAS 226
QY 240 AMSELKDAATKTLDASTKFTVSTDDALSFAIWKASRVRLERIDGSAFTEFCRAVDARPA 299
DB 227 KIKLRAKASRNL---VKNPTRVEAVTALFWRVCVKV--SRLSLTP----RTSVLQILV 277
QY 300 GVSNNYPGLLQNMVTHNSTIGEIANESLGATASRLSELDPASMRQRTGLATYILHNPD 359
DB 278 NLRGKVDLSLNTIGNMLSLMKNEE--AARIQDVVDEI---RRAKEIFSLNCKEWS 332
QY 360 KSNVSLTADADPSTSV-----MLSSWAKVGLWDYDFGLGCKPFTVRPIPEPVE 409
DB 333 KSSSRIFELLEIGKVYGRGNEMDLWMSNSWCKGLYDADF--GWGKPVWVTGRGTSHF 390
QY 410 SLMYFMPKPPDGEFCAA--LSLRDEMDRLKADKE 442
DB 391 NLMLLIDTK-DGEGIEAWITLITEQMSLFECDOE 423

RESULT 9
US-08-207-904-2
; Sequence 2, Application US/08207904
; Patent No. 5477002
; GENERAL INFORMATION:
; APPLICANT: Tuttle, AnnMarie
; APPLICANT: Crossland, Lyle D.
; TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic
; TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:


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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/207,904
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION NUMBER: US/07/908,242
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: CGC 1624
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-207-904-2

Query Match          5.7%; Score 134; DB 1; Length 448;
Best Local Similarity 21.7%; Pred. No. 6.2e-05;
Matches 104; Conservative 58; Mismatches 183; Indels 134; Gaps 24;

QY 21 TQISLLY-----PVSDSSQYPTIVSTFEGGLK-----FSEAVPWAGQVKAEG 64
DB 34 THVPTIYYRFFCHDCPLPSTDN-----IIKLTRSLSKALVHFYPLSGRLRWIAG-----S 83
QY 65 ISENGTGTGFIVPFEDPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENIAPR--KTL 122
DB 84 RLELDCNAGIVLMEAEATEAKLDLGLDFSP-----DLSLFPFVDYTI 128
QY 123 PIGPGTGPDDPKPVILLQL-NFIKGLIILTVNGQHGAMDMVGQDAVIRLLSKA--CRNDP 179
DB 129 PI-----DELPLLVQLTKFCGGIALSFAISHAVD--GQSALYFLTEWASLARGE 179
QY 180 FTEEMTAMNLDKRTI-----VPYLENTYTIGPEVDHQIVKADVAGDAVLTPVSASW 231
DB 180 LGNEPFP-----DRKFLRAGEPPIAYTTFEHLQFNP-----PPLLGGSS-- 220
QY 232 APFTSPKAMSELKDAATKTLDASTKFV-----STDDALSAPIWKSASRVRL 278
DB 221 -----EKKNETKGSMLKTKHQVEMLRKANQGNQGRSYTRYEVVTAHWRACKARG 275
QY 279 ERIDGSAPTEFCRAVDARPA--GVSNNTYPGLLQNNMTYHNTSTIGEANESLGATASRLRS 336
DB 276 HKFE--QPTNLCLICVNIQMPPPKSYFGNAIVDVIANGVSGDITSRPLEYVARRVR-- 332
QY 381 AKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMP-KKPDGEFCALSIRDEMDRLK 438
DB 384 ISLPLGLDPLGFWG---KEIHMSPTGTHEYDGDVCVILPFGKGGSLTVAIILQAVHVDFAK 439

RESULT 10
US-08-207-904-17
; Sequence 17, Application US/08207904
; Patent No. 5477002
; GENERAL INFORMATION:
; APPLICANT: Tuttle, AnnMarie
; APPLICANT: Crossland, Lyle D.
; TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic
; TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences
; NUMBER OF SEQUENCES: 21
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/207,904
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION NUMBER: US/07/908,242
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: CGC 1624
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-207-904-17
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Query Match          5.7%; Score 134; DB 1; Length 448;
Best Local Similarity 21.7%; Pred. No. 6.2e-05;
Matches 104; Conservative 58; Mismatches 183; Indels 134; Gaps 24;

QY 21 TQISLLY-----PVSDSSQYPTIVSTFEGGLK-----FSEAVPWAGQVKAEG 64
DB 34 THVPTIYYRFFCHDCPLPSTDN-----IIKLTRSLSKALVHFYPLSGRLRWIAG-----S 83
QY 65 ISENGTGTGFIVPFEDPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENIAPR--KTL 122
DB 84 RLELDCNAGIVLMEAEATEAKLDLGLDFSP-----DLSLFPFVDYTI 128
QY 123 PIGPGTGPDDPKPVILLQL-NFIKGLIILTVNGQHGAMDMVGQDAVIRLLSKA--CRNDP 179
DB 129 PI-----DELPLLVQLTKFCGGIALSFAISHAVD--GQSALYFLTEWASLARGE 179
QY 180 FTEEMTAMNLDKRTI-----VPYLENTYTIGPEVDHQIVKADVAGDAVLTPVSASW 231
DB 180 LGNEPFP-----DRKFLRAGEPPIAYTTFEHLQFNP-----PPLLGGSS-- 220
QY 232 APFTSPKAMSELKDAATKTLDASTKFV-----STDDALSAPIWKSASRVRL 278
DB 221 -----EKKNETKGSMLKTKHQVEMLRKANQGNQGRSYTRYEVVTAHWRACKARG 275
QY 279 ERIDGSAPTEFCRAVDARPA--GVSNNTYPGLLQNNMTYHNTSTIGEANESLGATASRLRS 336
DB 276 HKFE--QPTNLCLICVNIQMPPPKSYFGNAIVDVIANGVSGDITSRPLEYVARRVR-- 332
QY 337 ELDPASMRQTRGLAT-----YLHNNPDKNSVLSITAD-----ADPSTSVMLSSW 380
DB 333 -----AAIKMVTSDYANSTIDFLKNQEDLSKYQ---DIHAFRSKEGPFYGNPNLGI--SW 383
QY 381 AKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMP-KKPDGEFCALSIRDEMDRLK 438
DB 384 ISLPLGLDPLGFWG---KEIHMSPTGTHEYDGDVCVILPFGKGGSLTVAIILQAVHVDFAK 439

RESULT 11
US-09-457-046B-28
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Sequence 28, Application US/09457046B
Patent No. 6287835
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 439
TYPE: PRT
ORGANISM: Taxus cuspidata
US-09-457-046B-28

Query Match 5.7%; Score 132; DB 3; Length 439;
Best Local Similarity 20.0%; Pred. No. 9,7e-05;
Matches 90; Conservative 78; Mismatches 183; Indels 98; Gaps 21;

QY 5 IQLDTGQLPGLLSIYTOISLLYPVSDSSQVPTIVST-----FEQGLKRFSEAVPVVAGQ 59
DB 27 LQLSSIDLNPGLVGRGSIFFNALLIYNASPS---PTMISADPAKPIREALAKTILVYPPFAGR 83
QY 60 VK-----AEGISEGNTGTSFIIVPPEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMF 111
DB 84 LRETENDGLEVECTGE---GAMFLAMADNELSVLGDF--DDSNPSFQQL-----LF 130
QY 112 DENIAPRKTLPFGTGPDDPKPVILLQNLFIKGLILTVNGOGHGMVQDQAVIRLL 171
DB 131 -----SLPL--DTNFKLSLLVQVQTRPTCGFVGVSPFHGVCDCRGAAQAFKGL 179
QY 172 SKACRN-----DPFTEEBMTAMNLDRTKI--VPYLENTYITGPEVDHQ----- 225
DB 180 AEWARGEVKLSLEPIWNRELVKLD--DPKLOFFHFEFLRAPSIVEKIVQ----- 227
QY 226 PVSASWAFFTFSPKAMSELKDAATKTLDASTKVFSTDDALSFAFIKWSASRVRLERIDGSA 285
DB 228 -----TYFIIDPETINYIKQS---VMECKEFCSCSFVEASAMTW--IARTFAPQIPESE 276
QY 286 PTEFCRAVDARPAMPAGVSNYPGLQNMVTHNS--TIGIANESLGATASRLRS-----ELD 339
DB 277 YVKILFGMDMR-----NSFNPLPSGYGNSIGTACADVNVQDLSGLSLRAIMTIKKS 330
QY 340 PASMRORTGLATYLNHNPKNSVLTADADPSTSVMLSSWAKVGLMDYDFGLGLGKPE 399
DB 331 KVSINDNFKSRVV---KSELDVNNHNE---NVVAFADWSRLGDFDEVDFGNGNAVSVS 383
QY 400 VRRIPEFVESLM--YFM-----PKPDG 421
DB 384 ---PVQOOSALAMQNYFLFKPSKNPKDG 409

RESULT 12
US-09-457-046B-69
Sequence 69, Application US/09457046B
Patent No. 6287835
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 69
LENGTH: 451
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-457-046B-69

Query Match 5.6%; Score 130.5; DB 3; Length 451;
Best Local Similarity 21.7%; Pred. No. 0.00015;
Matches 99; Conservative 77; Mismatches 182; Indels 133; Gaps 26;

QY 4 KIQLDTLG--QLPGLLSIYTOISLLYP--VSDSSQVPTIVSTFEQGLK-----RSEAVPW 56
DB 23 RLQLSLDLIYCPG---IYVSTIFFYDLITSESE-----VFSENKLKLSLSETLSRFP--L 72
QY 57 AGOVKAEGISEGNTGTSFIIVPPEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENII 116
DB 73 AGRIGLSISCNDEGAVTEARTD---LLLPDFLRNLNTDLSLGF----- 114
QY 117 APRKTLP--IGPCTGPDPPKPVILLQNLFI--KGLILTVNGOGHGMVQDQAVIRLLSK 173
DB 115 -----LPTLAAGESP--AAWPLLISVKVTFPGSGGVAVSVSVSHKICDIALSVLTFVK----- 164

Matches 105; Conservative 64; Mismatches 195; Indels 119; Gaps 25;

QY 8 DTGQLPGLLSIYTOISLLYPVSDSSQVPTIVSTFEQGLKRFSEAVPVVAGVQK----- 61
DB 29 DOVGTHIPTLTLY-----FYDKPSESFOGNNVVEILLKLSRVLVHFYPMAGRLRWLPRGR 83
QY 62 -----AEGI-----SEGNTGTSFIIVPPEDVPRVVVKDLRDDPSAPTIEGMRKAGYPM 109
DB 84 FELNCNAREGVEFTEASEGK-----LSDFKDFSPTEFENL----- 119
QY 110 MFENIAPRKTLPFGTGPDDPKPVILLQNLFIK--GGLILTVNGOGHGMVQDQAVI 168
DB 120 MPQVNYKNPIETIPL-----FLAQVTKFKCGGISUSVNVSHAIVD--GQSA--L 164
QY 169 RLIS---KACRNDPFTTEEMTAMNLDRTKI---VPYLENTYITGPEVDHQ----- 211
DB 165 HLISEWGLRARGEPL-----TVPFLDRKILWAGEP--LPPFVSPPKDFKHKEPDQPPFLICE 219
QY 212 --IVKADVAGGDVAVLTPVSASWAFFTFSPKAMSELKDA--TKTLDASTKVFSTDDALS 267
DB 220 TDNVEERKKXTIVVMLPLSTLS-----QLQKLRSKANGSKHSDPAKGF--TRYETVTG 269
QY 268 FIWKSASRVRLERIDGSAPTEFCRAVDARPAM--GVSNYPGLQNMVTHNSTIGIANE 325
DB 270 HWKSCACKAGH--SPQPTALGICIDTISRMEPPLPRGYFGNATLDVVAASTSGELISN 327
QY 326 SLGATASRLSELDPASMRORTGLATYLNHNPD--KSNVSLTA-----DADPSTSV 376
DB 328 ELGFAASLSKAIKNTVNEYVMIGI--EYLKNQKDLKKFQDLHALGSTEGFYGNPNLGV 386
QY 377 LSSWAKVGLMDYDFGLGLGKPEIVRRPIPEPVESLMVFP--KKPDGEFCALSLRDEMD 435
DB 387 --SWLTPMYGLDFGWG---KEFYTGPGTHDFGDSLLILPDQNGEDGSVILATCLQVAHME 441
QY 436 RLK 438
DB 442 AFK 444

RESULT 13
US-09-457-046B-60
Sequence 60, Application US/09457046B
Patent No. 6287835
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 60
LENGTH: 435
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-457-046B-60

Query Match 5.4%; Score 126.5; DB 3; Length 435;
Best Local Similarity 20.2%; Pred. No. 0.00036;
Matches 99; Conservative 77; Mismatches 182; Indels 133; Gaps 26;

QY 4 KIQLDTLG--QLPGLLSIYTOISLLYP--VSDSSQVPTIVSTFEQGLK-----RSEAVPW 56
DB 23 RLQLSLDLIYCPG---IYVSTIFFYDLITSESE-----VFSENKLKLSLSETLSRFP--L 72
QY 57 AGOVKAEGISEGNTGTSFIIVPPEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENII 116
DB 73 AGRIGLSISCNDEGAVTEARTD---LLLPDFLRNLNTDLSLGF----- 114
QY 117 APRKTLP--IGPCTGPDPPKPVILLQNLFI--KGLILTVNGOGHGMVQDQAVIRLLSK 173
DB 115 -----LPTLAAGESP--AAWPLLISVKVTFPGSGGVAVSVSVSHKICDIALSVLTFVK----- 164

QY 174 ACNDPTEBEEMTAMLDRTKIIVPYLYNTIGVEVDHQIVKADVAGDAVLTPVSASWAF 233
Db 165 ----DWAT-----TTAKGKSNTI-EFAETIIPPPSHMYEFPSTDSNIT-----SKYVL 213
QY 234 --FTFSPKAMSELK-DAATKTLDASTKFVSTDALSAFTWKS----- 273
Db 214 KRFVFPFKIAELKHKAASESVVPTRV-----BAIWSLIWRCARNSRSLIPROAVMW 269
QY 274 -----SRVLRBRIDGSAPTFCRAVDARPMGVSNPNYGLLQNMTHNSTIGEIA 323
Db 270 QAMDIRLRIPSSVAPKDVIGLQSGSLKKAASEBEI-----PEIVATFRKNKERNEMI 325
QY 324 NESLGATASRLSELDPASMRQTRGLATVYLNHPDKSNVSLTAD-ADPSTSV---MLSS 379
Db 326 KESLOG-----NTIGQSLLSLMAETVSESTEIDRYIMSS 359
QY 380 WAKVGLWDYDFGLGLGKPETV---RRPIPEVPSLMYFMPKDPDGEFCAALSURDDEMDR 436
Db 360 WCKRPYEVDF--GSGSPVWVGASHYTIYDVMGVVLIDSKEGDG-VEAWISLFEEDMSV 416
QY 437 LKADKEWTKYA 447
Db 417 FVDDQELLAYA 427

RESULT 14
US-09-457-046B-68
; Sequence 68, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457, 046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Catharanthus roseus
US-09-457-046B-68

Query Match 5.4%; Score 125.5; DB 3; Length 439;
Best Local Similarity 20.5%; Pred. No. 0.00046;
Matches 95; Conservative 75; Mismatches 193; Indels 101; Gaps 23;

QY 18 SIY---TQISLLYPVSDSSQYPIVSTFEQGL-KRFSEAVPWAGQVKAEGISEGNTGTS 73
Db 39 NIYTQCVSGVFFYENPDGIBISTIREQLQNSLTKLVSYYPFAGKVVKNDYIHCNDDGIE 98
QY 74 FIVPFEDVPRVVKDLRDDPSAPTIEGMRKAGYPMAFDENIAPRKTLPIGPGTGPDPP 133
Db 99 FV---EVRICRNDI-----LKTSLSYARDVLPRVT-----VSEDT 136
QY 134 KPVIQLQNFIKGGLITVNGQHGMDVMGQDAVIRLLSK-----ACRNDPTEBEEMTAM 188
Db 137 TAIVQLS-HFDCGGLAVAFGISH---KVADGGTIASFMKDAASAC-----YL 180
QY 189 NLDRTKIIVPYLYNTIGVEVDHQIVKADVAGDAVLTPVSASWA---FFTFSPKAMSELKD 246
Db 181 SSSHVPTPLLVSDSIFFPRQDNICEQ-----FPTSKNCVEKTFIPPEAIEKLK- 230
QY 247 AATKTLDASTKFKVSTDALSAFTWKS-----SRVLRIDGSAPTFCRAVDARPMGV 301
Db 231 --SKAVEFGIEKTRVEVLTAFLSRCATVAGKAANNCGQSLPPVLOAINLRFILEL 288
QY 302 SNNYPGLLQNMTHNSTIGEIANESLG-----ATASRLSELDPASMRQTRGLA---- 351
Db 289 PQNSVGNLVSI-YFSRTIKE--NDYLNKEYTKLVINELRKE-----KQIKNLSREKL 339
QY 352 TYLHNNPD-----KSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPKETVRPIF 405

Db 340 TYVAQMEEFVKSLEKEDISNFLDID---AYLSDSWCRFPFPDYDF--GWCKPIWV--CLF 392
QY 406 EPVESLMYFMPKKPDGE---FCAALSLRDEDMRLKADKEWTKY 446
Db 393 QPIKNCVVMDDYFPFGDDYGEIAIVSFEQEKSAFEKNEQLLP 436

RESULT 15
US-09-457-046B-73
; Sequence 73, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457, 046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-73

Query Match 5.3%; Score 124; DB 3; Length 445;
Best Local Similarity 19.6%; Pred. No. 0.00068;
Matches 93; Conservative 79; Mismatches 176; Indels 126; Gaps 23;

QY 20 YTOISLLYPVSDSSQ---YPTIVSTFEQGL-KRFSEA-VPW--VAGOVKAEG---ISE 67
Db 37 HTGAVLIYKOPNEDNIHPSMYPDANILIEALSALVPFPYPMAGRLKINGDRVEIDC 96
QY 68 GNTGTSFIVPFEDVPRVVKDLRDDPSAPTIEGMRKAGYPMAFDENIAPRKTLPIGPG 127
Db 97 NAEALFV---EASSHVLEDFG--FRPNDE-LHRVMVPTCDYSKGI----- 138
QY 128 TGPDDPKPVILLQL-NFIKGGILTVNGQHGMDVMG-----QDAV 167
Db 139 ----SSFPLLMVQLTRFCGGVSGIPAQHHVDCGMAHFEFNNSWARIAKGLLPALPEPVH 194
QY 168 IRLSKACNDPTEBEEMTAMLDRTKIIVPYLYNTIGVEVDHQIVKADVAGDAVLTPV 227
Db 195 DRYLHLRPRNP-----QIKYSHSQFEPFPVLPNELLDGK-----T 231
QY 228 SASWAFPTFSPKAMSELKDAATKTLDASTKFVSTDALSAFTWKSASRVRLERIDGSA 285
Db 232 NKSQTLFILSREQINTLK-----QKLDLSNNTTFLSTYEVVAHVRSVSKAR--GLSDHE 285
QY 286 PTEFCRAVDARPM-----GVSNYPGLLQNMTHNSTIGEIANESLGATASR----- 333
Db 286 EIKLIMPVDRGRSRINNPSPKPGYCGNVFLAVCTATVGLDLSCNPLTDTAGKVQEALKGLD 345
QY 334 ---LRSELDPASMRQTRGLATVYLNHPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDF 390
Db 346 DDLRSADHTESKP---GLVPYMGSPKTY-----PNVLVNSGRIPYQAMDF 393
QY 391 GLGLGKPKETVRPIPFVPSLMY-----FMPKKP-DGEFCAALSURDDEMDRLK 438
Db 394 GWG-----SPTFFGISNIFDGCFLIPSRDGGSGMTLAINLFSSLSRPF 439

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OM protein - protein search, using sw model

Run on: January 23, 2005, 19:49:13 ; Search time 84 Seconds
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Title: US-10-614-954-6
Perfect score: 2334
Sequence: 1 MAPK1QDITGLQGLLSIY.....EDMDRLKADKWTKYAQVIG 451

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Listing first 45 summaries

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 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2334	100.0	451	13	US-10-074-279-6
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4	1860.5	79.7	459	15	US-10-614-954-2
5	962.5	41.2	474	13	US-10-074-279-8
6	962.5	41.2	474	15	US-10-614-954-8
7	187.5	8.0	446	16	US-10-437-963-178429
8	176.5	7.6	446	17	US-10-425-115-345339
9	175.5	7.5	429	15	US-10-424-599-209286
10	173.5	7.4	475	15	US-10-425-114-47544
11	172.5	7.4	440	17	US-10-425-115-222381
12	172.5	7.4	445	16	US-10-437-963-130033
13	170.5	7.3	436	13	US-10-078-929-64

14	168.5	7.2	446	13	US-10-078-929-52	Sequence 52, Appl
15	168.5	7.2	446	17	US-10-423-115-283768	Sequence 283768,
16	166	7.1	449	16	US-10-437-963-178427	Sequence 178427,
17	165	7.1	468	13	US-10-437-963-146649	Sequence 146649,
18	161	6.9	439	13	US-10-078-929-60	Sequence 60, Appl
19	161	6.9	442	16	US-10-437-963-130353	Sequence 130353,
20	158.5	6.8	1887	16	US-10-437-963-143096	Sequence 143096,
21	158	6.8	466	16	US-10-437-963-179552	Sequence 179552,
22	157.5	6.7	431	16	US-10-437-963-164992	Sequence 164992,
23	156.5	6.7	448	15	US-10-424-599-261757	Sequence 261757,
24	155.5	6.7	394	16	US-10-437-963-200106	Sequence 200106,
25	155	6.6	460	17	US-10-739-930-9224	Sequence 9224, Ap
26	153.5	6.6	460	15	US-10-425-114-46265	Sequence 46265, A
27	152.5	6.5	465	15	US-10-424-599-154573	Sequence 154573,
28	148	6.3	436	17	US-10-425-115-255718	Sequence 255718,
29	147.5	6.3	458	16	US-10-437-963-123563	Sequence 123563,
30	146	6.3	499	17	US-10-425-115-294646	Sequence 294646,
31	146	6.3	504	15	US-10-425-114-57512	Sequence 57512, A
32	144.5	6.2	833	16	US-10-437-963-130430	Sequence 130430,
33	144	6.2	431	13	US-10-078-929-200	Sequence 200, App
34	143	6.1	449	16	US-10-437-963-108868	Sequence 108868,
35	142.5	6.1	457	15	US-10-424-599-277367	Sequence 277367,
36	142	6.1	448	9	US-09-866-572A-56	Sequence 56, Appl
37	142	6.1	448	9	US-09-866-570A-56	Sequence 56, Appl
38	142	6.1	448	14	US-10-166-984-58	Sequence 56, Appl
39	142	6.1	448	15	US-10-166-984-56	Sequence 56, Appl
40	141.5	6.1	436	9	US-09-866-572A-62	Sequence 62, Appl
41	141.5	6.1	436	9	US-09-866-570A-62	Sequence 62, Appl
42	141.5	6.1	436	14	US-10-166-984-62	Sequence 62, Appl
43	141.5	6.1	436	15	US-10-166-984-62	Sequence 62, Appl
44	141.5	6.1	483	16	US-10-437-963-200505	Sequence 200505,
45	140	6.0	447	16	US-10-437-963-168477	Sequence 168477,

ALIGNMENTS

RESULT 1

US-10-074-279-6
; Sequence 6, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence1ist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Fusarium graminearum
US-10-074-279-6

Query Match	100.0%	Score 2334;	DB 13;	Length 451;
Best Local Similarity	100.0%	Pred. No. 4.2e-203;		
Matches 451;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	MAPK1QDITGLQGLLSIYQTISLLYPVSDSQYPTIVSTFPQGLKRFSEAPVWAGQV	60	
Db	1	MAPK1QDITGLQGLLSIYQTISLLYPVSDSQYPTIVSTFPQGLKRFSEAPVWAGQV	60	
Qy	61	KAEGISGNTGTSFIYPFDVPRVVVKDLRDDPSAFTIEGMRKAGYPMAFDENIAPRK	120	

Db 61 KAEGISEGNTGTSFIVPPEDVPRVVVKDLRDDPSAPTEIEGMRKAGYPMAMFDENIIAPRK 120
Qy 121 TLPFGTGPDPKPVILLQNLNFIKGLILTVNGQHGMVMGQDAVIRLLSKACRNDPF 180
Db 121 TLPFGTGPDPKPVILLQNLNFIKGLILTVNGQHGMVMGQDAVIRLLSKACRNDPF 180
Qy 181 TEEMTAMNLDRTIIVPYLENTTIGPEVDHQIVKADVAGGDVILTPVSASWAFFTFSPKA 240
Db 181 TEEMTAMNLDRTIIVPYLENTTIGPEVDHQIVKADVAGGDVILTPVSASWAFFTFSPKA 240
Qy 241 MSELKDAATKTLDASTKPVSTDDALSFAITWKSASRVRLERIDGSAPTEFCRAVDARPMAG 300
Db 241 MSELKDAATKTLDASTKPVSTDDALSFAITWKSASRVRLERIDGSAPTEFCRAVDARPMAG 300
Qy 301 VSNYPGLLQNMTHNSTTIGETANESLGATASRLSELDPASNRQTRGLATYLHNNPDK 360
Db 301 VSNYPGLLQNMTHNSTTIGETANESLGATASRLSELDPASNRQTRGLATYLHNNPDK 360
Qy 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPKETVRRPIPEPVESLMYFMPKKPD 420
Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPKETVRRPIPEPVESLMYFMPKKPD 420
Qy 421 GEFAALSRLDEDMRLKADKEWTKYAQYVG 451
Db 421 GEFAALSRLDEDMRLKADKEWTKYAQYVG 451

RESULT 2

US-10-614-954-6
; Sequence 6, Application US/10614954
; Publication No. US20040034884A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/614,954
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Fusarium graminearum
US-10-614-954-6

Query Match 100.0%; Score 2334; DB 15; Length 451;
Best Local Similarity 100.0%; Pred. No. 4.2e-203;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAFKIQDLTGQPLGILLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60
Db 1 MAFKIQDLTGQPLGILLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60
Qy 61 KAEGISEGNTGTSFIVPPEDVPRVVVKDLRDDPSAPTEIEGMRKAGYPMAMFDENIIAPRK 120
Db 61 KAEGISEGNTGTSFIVPPEDVPRVVVKDLRDDPSAPTEIEGMRKAGYPMAMFDENIIAPRK 120
Qy 121 TLPFGTGPDPKPVILLQNLNFIKGLILTVNGQHGMVMGQDAVIRLLSKACRNDPF 180
Db 121 TLPFGTGPDPKPVILLQNLNFIKGLILTVNGQHGMVMGQDAVIRLLSKACRNDPF 180
Qy 181 TEEMTAMNLDRTIIVPYLENTTIGPEVDHQIVKADVAGGDVILTPVSASWAFFTFSPKA 240
Db 181 TEEMTAMNLDRTIIVPYLENTTIGPEVDHQIVKADVAGGDVILTPVSASWAFFTFSPKA 240

Qy 241 MSELKDAATKTLDASTKPVSTDDALSFAITWKSASRVRLERIDGSAPTEFCRAVDARPMAG 300
Db 241 MSELKDAATKTLDASTKPVSTDDALSFAITWKSASRVRLERIDGSAPTEFCRAVDARPMAG 300
Qy 301 VSNYPGLLQNMTHNSTTIGETANESLGATASRLSELDPASNRQTRGLATYLHNNPDK 360
Db 301 VSNYPGLLQNMTHNSTTIGETANESLGATASRLSELDPASNRQTRGLATYLHNNPDK 360
Qy 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPKETVRRPIPEPVESLMYFMPKKPD 420
Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPKETVRRPIPEPVESLMYFMPKKPD 420
Qy 421 GEFAALSRLDEDMRLKADKEWTKYAQYVG 451
Db 421 GEFAALSRLDEDMRLKADKEWTKYAQYVG 451

RESULT 3

US-10-074-279-2
; Sequence 2, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Fusarium sporotrichioides
US-10-074-279-2

Query Match 79.7%; Score 1860.5; DB 13; Length 459;
Best Local Similarity 77.6%; Pred. No. 4.8e-160;
Matches 349; Conservative 50; Mismatches 50; Indels 1; Gaps 1;

Qy 2 AFKIQDLTGQPLGILLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 61
Db 11 SFDIELDIITGQOPLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRLSQTFFWAGQV 70
Qy 62 ARGISEGNTGTSFIVPPEDVPRVVVKDLRDDPSAPTEIEGMRKAGYPMAMFDENIIAPRK 121
Db 71 TEGISEGNTGTSKIIPYESTPLRVVKDLRDDSSAPTEIEGLRKAGPPELVVAPRK 130
Qy 122 LPIPGTGPDPKPVILLQNLNFIKGLILTVNGQHGMVMGQDAVIRLLSKACRNDPF 181
Db 131 LAIGPENGNDPKPVILLQNLNFIKGLILTVNGQHGMVMDTDALIRLLSKACRNEST 190
Qy 182 EREMTAMNLDRTIIVPYLENTTIGPEVDHQIVKADVAGGDVILTPVSASWAFFTFSPKAM 241
Db 191 EBEISANNLDRTIIVPYLENTTIGPEVDHQIVKADVAGGDVILTPVSASWAFFTFSPKAL 249
Qy 242 SELKDAATKTLDASTKPVSTDDALSFAITWKSASRVRLERIDGSAPTEFCRAVDARPMAGV 301
Db 250 SELKDAATKTLDASSKPVSTDDALSFAITWQSTSRVRLARLDASTTEFCRAVDMRGPMGV 309
Qy 302 VSNYPGLLQNMTHNSTTIGETANESLGATASRLSELDPASNRQTRGLATYLHNNPDKS 361
Db 310 SSTYPGLLQNMTHYDSTVAEIANEPUGATASRLSELDSRLRRRTQALATWHLGLPDKS 369
Qy 362 NVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPKETVRRPIPEPVESLMYFMPKKPDG 421

Db 370 SVSLTADANPSSIMLSSWAKVCCWEYDFGFLGKPESVRRPRPEFESLMYFMPKPKDG 429
QY 422 EFCALSLRDEDMRLKADKEMTKYAYVG 451
Db 430 EFTASISLRDEDMERLKADKEWTKYAKYIG 459

RESULT 4

US-10-614-954-2
; Sequence 2, Application US/10614954
; Publication No. US20040034884A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmerson, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/614,954
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Fusarium sporotrichioides
US-10-614-954-2

Query Match 79.7%; Score 1860.5; DB 15; Length 459;
Best Local Similarity 77.6%; Pred. No. 4.8e-160;
Matches 349; Conservative 50; Mismatches 50; Indels 1; Gaps 1;
QY 2 AFKIQDITGQLPGLLSIYTOISLLYPVSDSSQYPTIVSTFEGLKRFSEAVPWVAGQVK 61
Db 11 SFDIELDIIGQQPGLLSIYTOISLLYPVSDSSQYPTIVSTFEGLKRLSQTFFPWVAGQVK 70
QY 62 AGGISGNTGTSFIVPFEDVPRVVKDLRDDPSAPTEIEGRKAGYPMAMFENIAPRKT 121
Db 71 TEGISEGNTGTSKIIPYETPRVVKDLRDDPSAPTEIEGRKAGYPMAMFENIAPRKT 130
QY 122 LPTGPGTDPDPKPVILLQNFILKGLILTVNGOHGMDVGDVIRLLSKACRNDPPT 181
Db 131 LAIFPGNGFNDKPVILLQNFILKGLILTVNGOHGMDVGDVIRLLSKACRNEST 190
QY 182 EEMTAMNLDKRTIVPYLENTYIGPRVDHQIVKADVAGDAVLTVPVSAWAFPTFSPKAM 241
Db 191 EEEISAMNLDKRTIVPYLENTYIGPRVDHQIVKADVAGDAVLTVPVSAWAFPTFSPKAL 249
QY 242 SELKDAATKTLDASTFVSTDDALSAPFINKSASRVRLERIDGSAFTEFCRAVDARPMGV 301
Db 250 SELKDAATKTLDASTFVSTDDALSAPFINKSASRVRLERIDGSAFTEFCRAVDARPMGV 309
QY 302 SNNYPGLQNMVTHNSTIGIEANESLGATASRLRSELDPASMRQRTKGLATYLLHNPDKS 361
Db 310 SSTYPGLQNMVTHNSTIGIEANESLGATASRLRSELDPASMRQRTKGLATYLLHNPDKS 369
QY 362 NVSLTADADPSTVMSLSSWAKVGLWDYDFGLGKGPETVRRPIFEPPVESLMYFMPKPKDG 421
Db 370 SVSLTADANPSSIMLSSWAKVCCWEYDFGFLGKPESVRRPRPEFESLMYFMPKPKDG 429
QY 422 EFCALSLRDEDMRLKADKEMTKYAYVG 451
Db 430 EFTASISLRDEDMERLKADKEWTKYAKYIG 459

RESULT 5

US-10-074-279-8
; Sequence 8, Application US/10074279

; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmerson, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-074-279-8

Query Match 41.2%; Score 962.5; DB 13; Length 474;
Best Local Similarity 44.4%; Pred. No. 2.2e-78;
Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;
QY 6 QLDITGQLPGLLSIYTOISLLYPVSDSSQYPTIVSTFEGLKRFSEAVPWVAGQVKAEGI 65
Db 22 QLDITGQLPGLLSIYTOISLLYPVSDSSQYPTIVSTFEGLKRFSEAVPWVAGQVKAEGI 81
QY 66 SEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTEIEGRKAGYPMAMFENIAPRKT-PI 124
Db 82 DEGNTGTYRIVPSDKIP-LIVQDLREDLSAPTMSLEKADFFIYMLDEKTFAPCMTINPP 140
QY 125 GPGTG-PDDPKPVILLQNFILKGLILTVNGOHGMDVGDVIRLLSKACRNDPTEE 163
Db 141 GMTIGMAKSGPVFAVQANFISGGLVLTIVGQHNINDITGQESIIINLLKSKCHQKPFSD 200
QY 184 EMTAMNLDKRTIVPYLENTYIGPRVD-HQIVKA--DVAGGDAVLTVPVSAWAFPTFSP 238
Db 201 ELLIGNIDKSKIPFDE-TWEPDITLVEHIVETSRTSNTSGEKEQSCSSNSTWAYVEFSA 259
QY 239 KAMSELKDAATKTLDASTFVSTDDALSAPFINKSASRVRLERIDGSAFTEFCRAVDARPA 298
Db 260 ISLQNLRIILAMQTCSTGTFVSTDDIVTAFIWKSVSRARLSRLKPKETKSNLGRAVDVYKR 319
QY 299 MGVSNNYPGLQNMVTHNSTIGIEANESLGATASRLRSELDPA--SMRQRTKGLATYLLHN 356
Db 320 LGLPETYPGLQNMVTHNSTIGIEANESLGATASRLRSELDPA--SMRQRTKGLATYLLHN 379
QY 357 NPDKSNVSLTADADPSTVMSLSSWAKVGLWDYDFGLGKGPETVRRPIFEPPVESLMYFMP 416
Db 380 CPDKTKVSIQPDITLSDGIMVSSWAKVLYDVFNLGLGKPKSVRRPRFISLESLEYFMP 439
QY 417 KXPDGFECAALSRLRDEDMRLKADKEMTKYAYVG 451
Db 440 RSSRGEMVVALCLRDKDECLNADKEWTKYATHIG 474

RESULT 6

US-10-614-954-8
; Sequence 8, Application US/10614954
; Publication No. US20040034884A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmerson, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods

```

; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/614,954
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-10-614-954-8

Query Match
Best Local Similarity 41.2%; Score 962.5; DB 15; Length 474;
Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;

QY 6 QLDLTLQGLLSIYTOISLLYVPVSDSSOYPTIVSTFEQGLKRFSEAVPWVAGQVKAEGI 65
DB 22 QLDLTLQGLLSIYTOISLLYVPVSDSSOYPTIVSTFEQGLKRFSEAVPWVAGQVKAEGI 81
QY 66 SEGNTGTSFTVPEDVPRVVVKDLRDDPSAPTIIEGMRKAGYPMAMPDENIIAPKTL-PI 124
DB 82 DEGNTGTYRIVPSDKIP-LIVQDLREDLSAPTMDSEKADFFIYMLDEKTFAPCMTINPP 140
QY 125 GPTG-PDDPKVILLQOLNFIKGLLITVNGQHGAMDMVQDAVIRLLSKACRNPFTEE 183
DB 141 GNTIGMAKSGPVFAVQANFISGLGLTIVGQHNIMDITGOSSINLLNKSCHQKPFSE 200
QY 184 EMTAMNLDRTIIVPLENTYIGPEVD--HOIVKA--DVAGGDVAVLTPVS-ASWAFPTFSP 238
DB 201 ELIIGNIDKSKSLPLFDE-TWEPDTLIVHEIVTSRTSGEEKQSCSSNIAWYVESA 259
QY 239 KAMSELKDAATKTLDASTKFSVSTDDALSAPFVKSASRVRLERIDGSAFTEFCRAVDARPA 298
DB 260 ISLQNLRIILAMQICTSGTKFVSTDDIVTAFVKSASRVRLERIDGSAFTEFCRAVDARPA 319
QY 299 MGVSNNYFGLLQNTVHNSITGIESLGATASRLSELDPA--SMQRTGLATYLNH 356
DB 320 LGLPETYFGLLVNMTFTGSLKSLDHSKGLVILASQIRKLDPKVDFLYNTCALATLLSR 379
QY 357 NPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVRRPPIPEPVESLMYFMP 416
DB 380 CPDKTKVSIQPIDTLGSIWSSWAKVSLYDVFNLGLGKPKSVRRPRFISLSLYFMP 439
QY 417 KPDPGEFCAALSURDEMDRLKADKEWTKYQVIG 451
DB 440 RSSRGEVMVALCLRDCKDWECLNADKEWNTYATHIG 474

RESULT 7
US-10-437-963-178429
; Sequence 178429, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 178429
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Oryza sativa

; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/614,954
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-10-614-954-8

Query Match
Best Local Similarity 44.4%; Score 1042.5115; DB 16; Length 446;
Matches 115; Conservative 58; Mismatches 188; Indels 105; Gaps 25;

QY 21 TQISLLY---PVSDSSOYPTIVSTFEQGL-KRFSEAVPWVAGQVKAEGISEGNT----- 70
DB 40 TYISVIYAYRPPAPAN-----AALEAGLAKALIEYREW-AGRLGVDG--DGNRAILLND 90
QY 71 -GTSFIVPFEDVPRVVVKDLRDDPSAPTIIEGMRKAGYPMAMPDENIIAPKTLPIGPGTG 129
DB 91 GGARFEATADVTLDSVMPLK-----PTAE-----VLSLHP--S 122
QY 130 PDDPKVILLQOL-NFIKGLLITVNGQHGAMDMVQDAVIRLLSKACRN--DPFTEEM 185
DB 123 GDDAVELMLIQVTRFACGSLVVGTTQHIIVADGRATNFFFLAWSQATRGAAFPVPHDR 182
QY 186 TAMNLDRTIIVPLE-----NYTIGPEVDHQIVKADVAGGD---AVLTPVSASWAFPTFSP 238
DB 183 VSFAPRDT--PKVEFEHGRVGFPEKPYDDDEDVHASGGGDDDEVVINKVLSREF----- 235
QY 239 KAMSELKDAATKTLDASTKFSVSTDDALSAPFVKSASRVRLERIDGSAFTEFCRAVDARPA 298
DB 236 --ISKLSQASA---GAHRPYSTLQCVVAHLWRCMTKAR--GLDGRSTSVCIADVGRAR 289
QY 299 MG--VSNNYFGLLQNTVHNSITGIESLGATASRLSELDPA--SMQRTGLATYLNH- 355
DB 289 MSPVPDGYTGNVILMARPTATAGELVTRPLKHAVELINREV-----IRINDGYKSFIDF 344
QY 356 --NPDKSNVSLTADADP-----STSVMLSSWAKVGLWDYDFGLGKPEVRRPPIF----- 405
DB 345 ANSGAVEERLIVASADAAEMVLSNIEVDSMLRIPFYDLDDEGG-----RPFFTFPS 396
QY 406 -EPVESLMYFMPK-KPDGEFCAALSURDEMDRLK-----ADKEWT 444
DB 397 YLIPVEGLLILPSPFGDGVDAAYVPLPSRDMDFVFNCCYSFDKQOT 442

RESULT 8
US-10-425-115-345339
; Sequence 345339, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 345339
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_78117C.1.pap
; US-10-425-115-345339

Query Match
Best Local Similarity 7.6%; Score 176.5; DB 17; Length 446;
Matches 109; Conservative 58; Mismatches 218; Indels 61; Gaps 19;

QY 13 LPGLLSIYTIQISLLYVPVSDSSOYPTIVSTFEQGLKRFSEAVPWVAGQVKAEG-----ISEG 68
DB 40 LPYITFYNQKLLLYRA--APDFPDVARNMTAALADALRVFVFLAGRIQDDGALAVEG 97
QY 69 NTGTSFTVPFE-DVPRVVVKDLRDDPSAPTIIEGMRKAGYPMAMPDENIIAPKTLPIGPG 127
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; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/614,954
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-10-614-954-8

Query Match
Best Local Similarity 41.2%; Score 962.5; DB 15; Length 474;
Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;

QY 6 QLDLTLQGLLSIYTOISLLYVPVSDSSOYPTIVSTFEQGLKRFSEAVPWVAGQVKAEGI 65
DB 22 QLDLTLQGLLSIYTOISLLYVPVSDSSOYPTIVSTFEQGLKRFSEAVPWVAGQVKAEGI 81
QY 66 SEGNTGTSFTVPEDVPRVVVKDLRDDPSAPTIIEGMRKAGYPMAMPDENIIAPKTL-PI 124
DB 82 DEGNTGTYRIVPSDKIP-LIVQDLREDLSAPTMDSEKADFFIYMLDEKTFAPCMTINPP 140
QY 125 GPTG-PDDPKVILLQOLNFIKGLLITVNGQHGAMDMVQDAVIRLLSKACRNPFTEE 183
DB 141 GNTIGMAKSGPVFAVQANFISGLGLTIVGQHNIMDITGOSSINLLNKSCHQKPFSE 200
QY 184 EMTAMNLDRTIIVPLENTYIGPEVD--HOIVKA--DVAGGDVAVLTPVS-ASWAFPTFSP 238
DB 201 ELIIGNIDKSKSLPLFDE-TWEPDTLIVHEIVTSRTSGEEKQSCSSNIAWYVESA 259
QY 239 KAMSELKDAATKTLDASTKFSVSTDDALSAPFVKSASRVRLERIDGSAFTEFCRAVDARPA 298
DB 260 ISLQNLRIILAMQICTSGTKFVSTDDIVTAFVKSASRVRLERIDGSAFTEFCRAVDARPA 319
QY 299 MGVSNNYFGLLQNTVHNSITGIESLGATASRLSELDPA--SMQRTGLATYLNH 356
DB 320 LGLPETYFGLLVNMTFTGSLKSLDHSKGLVILASQIRKLDPKVDFLYNTCALATLLSR 379
QY 357 NPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVRRPPIPEPVESLMYFMP 416
DB 380 CPDKTKVSIQPIDTLGSIWSSWAKVSLYDVFNLGLGKPKSVRRPRFISLSLYFMP 439
QY 417 KPDPGEFCAALSURDEMDRLKADKEWTKYQVIG 451
DB 440 RSSRGEVMVALCLRDCKDWECLNADKEWNTYATHIG 474

RESULT 7
US-10-437-963-178429
; Sequence 178429, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 178429
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Oryza sativa
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Db 98 DEGAEV---FEAEOGVAVDDL-----AGGDCS--DE---AEKVQLHLVPY 135
QY 128 TGDDP---PKPVILLQNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTTE 183
Db 136 TGVNLEGLRPLLAQVFTKLDGLAVGACAFNHAVIDGTSTWHFMSWAEKRGVPLSLQ 195
QY 184 ENTAMNLDKRTIIVYLENTYIGPEVDHQIVKADVAGDAVLTPVVSASMAFFTFSPKAMSE 243
Db 196 PIHDRSLRSVRV-RLEL-----PASAEAEKTDPNPKKALVA-----RVFSPEPTVAR 245
QY 244 LKDAATKTLDASTKFTVSTDDALSFAFWKSASRVRLRIDGSAP---TEFCRAVDARPAMG 300
Db 246 IKAANAALPPGAKPFTSQSGAHWRAVSRAR-----GLGPADITAFVAFDCAERLD 300
QY 301 --VSNYPGLLQNMTHNSTIGBIANESLGATASRLSELDPASMRQRTGLATYLHNPN 358
Db 301 PPLPAYFGLNLOAVFTGVPAGMLLGGPPPELPAQLQKALDEHDAADAATVRLSEY-EAP 359
QY 359 DKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKGPETVRRPIPEPVESLMYPMP-K 417
Db 360 KLFHYS---DAGPN-CVAVGSSPRFRVYDVF--GFRPERSVRSNGGNKFDGMVILYPCR 413
QY 418 KPDGEFCAALSRLDEDMRLKADKEW 443
Db 414 GGGGIDVELALQPEPMQRLKDDDF 439
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RESULT 9

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US-10-424-599-209286
; Sequence 209286, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 209286
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_31012C.1.pap
US-10-424-599-209286
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Query Match 7.5%; Score 175.5; DB 15; Length 429;
Best Local Similarity 22.2%; Pred. No. 6.7e-07;
Matches 103; Conservative 67; Mismatches 183; Indels 111; Gaps 22;
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QY 21 TQISLYPVSDSSQYPTIVSTFEGGLKRFSEAVPWVAGQVKAEGISEGNTGTSFIVFP-- 78
Db 25 SNVDLVPP---NPHTPSVFYRSNGAPNFPD-----GKVMKEAL-----TKVLVPFPY 69
QY 79 -----EDVPRV-----VVKDLRDDPSAPTIEGMRKAGYPMAMFDE 113
Db 70 MAGRLRDDDDGRVEIDCDGGGVLFVEADTGAVIDDFGD--FAPTLR-LRQL-IPAVDYSQ 125
QY 114 NIAPRKTLPFGTGPDPDPKPVILLQLNFIK--GGILTVNGQHGAMDMVGQDAVIRLLS 172
Db 126 GIAS-----YPLLVLQVTHFKCGVSLGVGMQHADVAGSLHFTNTWS 169
QY 173 KACRNDPFTTEEMTNMLDKRTIIVYLENTYI-----GPEVDHQIVKADVAGDAVLTP 226
Db 170 DVAR-----GLD-VSIPPPFDRTILRADPPRPIFDHIEYKPPPMKTTQOATN 216
QY 227 VSASMAFFTFSPKAMSELKDAATKTLDASTKFTVSTDDALSFAFWKSASRVRLRIDGSAP 286
```

```
Db 217 ASAAVSIFLTRDQLNTLK--AKSKEDGNTIISYSSVEMLAGHVRSVSKAR--ALPDDQE 272
QY 287 TEFCAVDARPAMGVSNYPGLLQNMTHNSTI---GEIANESLGATASRLSELDPASM 343
Db 273 TKLYIATDGRSLQPPTP--PGYFGNVIFTTPIAVAGDLSMKTWYASRIHNAL---L 327
QY 344 RORT---RGLATYLHNPNPKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETV 400
Db 328 RMDNDYLSALDYLELQPDLKALVRGAHTFKCPNLGITSWRLPIHDADFGWG----- 380
QY 401 RRIPE-----PVESLMYEMPKP--DGEFCAALSRLDEDMRLK 438
Db 381 -RPIFMGPGIAYEGLSFIIPSTNDGSLVAIALQPDHMKLFK 423

RESULT 10
US-10-425-114-47544
; Sequence 47544, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaka, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 47544
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700071662_FLI.pap
US-10-425-114-47544
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Query Match 7.4%; Score 173.5; DB 15; Length 475;
Best Local Similarity 21.0%; Pred. No. 1.2e-06;
Matches 98; Conservative 59; Mismatches 157; Indels 153; Gaps 19;
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QY 69 NTGTSFIVPEFEDVPRVVKDLRDDPSAPTIEG-----NRKA-----GYPMA----- 109
Db 59 NSNLDLVPRFHTPSVYF--YRRDGPVPAEAGFFDGERMRRALAEALVPFYPMAGRLARD 116
QY 110 -----MFDENIATP-----RKTLPFGTGPDDPKPVILQ 140
Db 117 EDRVEIDCNGEGLVFVEADAPDASVDDYGDFAPTMELKRLIPTVDYTDIDISAPFLVLQ 176
QY 141 LNFIK--GGILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTTEEMTNMLDKRTIVPYL 199
Db 177 VYFKCGVSLGVGMQHHAADGMSGLHFINSDLCRG----- 214
QY 200 ENYTIPEVDHQIVKADVAGDAVLTPVVSASMAFFTFSPKAMSELKDAATKTLDASTKVF 259
Db 215 AQISVMPFIDRTLRA-----RDPTPSFQHIEYQP-----APAMLSSTTQPL 257
QY 260 -----STDDALSFAFWKSASRVRLERID 282
Db 258 ASKSKPPATAVDIFKLTURSDGLRLSQLPAGEAPRFTSYAVLAHVWKVCVSLAR--SLP 315
QY 283 GSAPTEFCRAVDARPAM--GVSNYPGLLQNMTHNSTI---GEIANESLGATASRLSE 337
Db 316 PPOPTKLYCATGQRQLQPLPDGVFG---NVIFATPLAEAGKVTS--LAEGAIVQGA 371
QY 338 LDPASMRQRTGLATYLHNPNPKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGK 397
Db 372 LDMD-NDYCRSALDYLELQPDLSALVRGAHTFRCFNLGLTSVRLPIHDADFGWG--- 426
QY 398 ETVRRIPE-----PVESLMYFMPK--KPDGEFCAALSRLDEDMRLK 438
```

APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 130033
LENGTH: 445
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_32232C.1.pap
US-10-437-963-130033

Query Match 7.4%; Score 172.5; DB 16; Length 445;
Best Local Similarity 22.8%; Pred. No. 1.3e-06;
Matches 110; Conservative 66; Mismatches 198; Indels 109; Gaps 21;

QY 2 AFKIQDITLQGLLSIYTOISLLYPV-SDSSOYPTIVSTFEQGLKRFSEAVPW---VA 57
DB 25 AAKCVLATF-DLPYITFYVQKLLLYLPLNGCASDFPDVAARMSASL---SDALAYFYFLA 80
QY 58 GQVKAEE---GIS-EGNTGTSTFIVPFEDVPRVVVKDLRDDPSAPTEIEGMRKAGYPMAMFD 112
DB 81 GRIRQDDHDSLSIHGQGAIEASAD--HVSVDQLAGEECSEAEKVMQL-----130
QY 113 ENITAPKTLPIGPGTGPDD---PKPVILLQALFIKGLLITVNGOGHGMVQGDAMI 168
DB 131 -----LVPTGYMNLGNRLPLAVQLTRLDGVAVGCAFNHVLDTGTSTWHFM 179
QY 169 RLKSKACRND-----PFTEE--EMTAMNLDKRTIVPYLENT 203
DB 180 TSWAELCHGGGAPSLPVHNRGMARSVRVNLPLASAEAEKTDPN-----225
QY 204 IGPEVDHIVKADVAGGDAVLTVPVSASWAFPTFSPKAMSELKDAATKTLASTKVFVSTDD 263
DB 226 -GPKV-----PLVA--RVFSFPSPSARAKAANAALPPGAKFPFSFQ 265
QY 264 ALSAIFWKSASRVRLERIDGSAPTEFCRAVDARPAWG--VSNNTYPGLLQNNYTHNSTIGE 321
DB 266 SLAAHIWRAVSRAR--ALGPSDITVFAVFAACRAELSPPLPAYFGNLIQAVFTGVPAGM 323
QY 322 IANESLGATASRLRSELDPASMRQRTGLATVYLNHNPKSNVSLTADADPSTVMSLSSWA 381
DB 324 LLAGPPELAAGLLQKAIIDHDAATRRLEERY-EAAPKLFHYS---DAGPN-CVAVGSSP 378
QY 382 KYGLWDYDFGLGKGPETVRRPIFEPVESLWYFMP-KKPDGFECAALSRLDEMDRLKAD 440
DB 379 RFRVYDVDF--GFRGPERVRSKANNKFDGMVLYLPGRGDGGIDVELSLQPEPMQRLDKD 436
QY 441 KEW 443
DB 437 QDF 439

RESULT 13
US-10-078-929-64
Sequence 64, Application US/10078929
Publication No. US20020152497A1
GENERAL INFORMATION:
APPLICANT: Rafalski, Antoni
APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio Carl
APPLICANT: Sakai, Hajime
APPLICANT: Famodu, Omolayo O.
APPLICANT: Odell, Joan T.
APPLICANT: Meyers, Blake
APPLICANT: Thorpe, Catherine
APPLICANT: Weng, Zude

APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 130033
LENGTH: 445
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_32232C.1.pap
US-10-437-963-130033

Query Match 7.4%; Score 172.5; DB 17; Length 440;
Best Local Similarity 21.7%; Pred. No. 1.3e-06;
Matches 96; Conservative 67; Mismatches 175; Indels 105; Gaps 20;

QY 69 NTGTSFIVPEDVPRVVVKDLRDDPSAPTEIEG-----MRKA-----GYPMA-----109
DB 24 NSNLDLVPRFHTSVTF--YRRDGPVPAEAGFFDGERMRRLAALVFPYPMAGRLARD 81
QY 110 -----MFDENIAP-----RKTLPFGPGTGPDDPKPVILLO 140
DB 82 EDGREVIDCNGEGLVFEADAPDASVDYDGFAPFTWELKRLIPTVDYTDIDISAPFLVLQ 141
QY 141 LNFYK-GGLIITVNGHGMVQGDAMIIRLLSKACRNDPFTSEMTAMNLDKRTIVPYL 199
DB 142 VTYFKCGVSLGVGMQHAADGMSGLHFINSWSDLCRGAQI-----SVWPF 188
QY 200 ENYITIG-----PEVDHIVKADVAGGDAVLT-----PVSASWAFPTFSPKAMSELKD 246
DB 189 DRTLRLARDPPTPSFQHFIEVQSAPAMLSSTQFLASKSKPATAVDIFKLTSLDLGLRL- 247
QY 247 AATKTLASTKVFSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAWG--GVSN 304
DB 248 SQLPAGEAPRF-STYAVLAHVWKCVSAR--SLPPEQPTKLYCATDGRQLPPLPDG 304
QY 305 YPGLLQNNYTHNSTI---GETANESLGATASRLRSELDPASMRQRTGLATVYLNHNPKDS 361
DB 305 YFG---NVIFTATPLAEGKVTSB-LAEGRAVIOGALDRMD-NDYCSALDYLELOPDL 359
QY 362 NVSLTADADPSTVMSLSSWAKVGLWDYDFGLGKGPETVRRPIFE-----PVSLSWYFMP 416
DB 360 ALVRCAHTFRCNGLTSLVRLPIHDADFQWG-----RPVPMGPGIAYEGLAFVLP 411
QY 417 K-KPDGFECAALSRLDEMDRLK 438
DB 412 SANGDGSLSIAISLQAEHMEKFR 434

RESULT 12
US-10-437-963-130033
Sequence 130033, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei


```
RESULT 15
US-10-425-115-283768
; Sequence 283768, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 283768
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_21897C.1.pep
US-10-425-115-283768

Query Match      7.2%; Score 168.5; DB 17; Length 446;
Best Local Similarity 21.8%; Pred. No. 3.le-06;
Matches 98; Conservative 63; Mismatches 177; Indels 111; Gaps 21;

QY 69 NTGTSPIVPFEDVRVVVKDLRDDPSAPTIEG-----MRKA-----GYPMA-- 109
Db 24 NSGPDLVVFRFHTPSYFP-FREDADGNDLAGADSGFFDGARMRRAALVFFYPMAGR 82
QY 110 -----MFDE-----NIAP-----RKTLPIGGTGPDPPKPV 136
Db 83 LARDEGRVEIDCAGGVLFQADAPDATIDYFGDFAPTMLKRLIPTVDFDDISSFPL 142
QY 137 ILLQLNFIK-GGLILTVNGHGMVMQGDVIRLLSKACRNDPFTTEEWTAANLDRKTI 195
Db 143 LVLQVTHFKCGGVAIGVQGHVADGFGSLHFINSWADLCRGVPI-----AV 189
QY 196 VPYLENTYIG-----PEVDHQIVKADVA-GGDAVLTPVSA-----SWAFFTFSPKAM 241
Db 190 MPFIDRLRLARDPPPTPAYPHIEYQAPAPMLSEPPQOALTSKEATPTTAVAIKLSRAEL 249
QY 242 SELKDAATKTLDASTKFSVSTDDALSAFIWKASRVRLERIDGSAPTEFCRAVDARPAMGV 301
Db 250 VRLR-SQVPARECAPRF-STYAVLAHVWRCSLAR--GLPADQPTKLYCATDGRQL-- 303
QY 302 SNNYP-----GLLQNMTHNSTIGEIANESIGAT--ASRLRSELDPASMEQRTGLATYLH 355
Db 304 ---QPPLPEGYFGNVITATPLANAGTGTAGVAGASVIOAALDRMD-DGYCRSALDYLE 359
QY 356 NNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGPKETVRRPIFE-----PVES 410
Db 360 LQPDLSALVRGAHTFCPNLGLTSWVRLPIHDADFCWG-----RPVFMGGGIAYEG 411
QY 411 LMYFMFK-KPDGEFCAALSDEDMRLK 438
Db 412 LAFVLPANRSGSLSLVAISLQAEHMEKFR 440
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Search completed: January 23, 2005, 19:55:39
Job time : 87 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 24, 2005, 01:40:16 ; Search time 6057 Seconds
(without alignments)
3521.158 Million cell updates/sec

Title: US-10-614-954-6
Perfect score: 2334
Sequence: 1 MAFKIQDTLQGLGLSIY.....EDMDRLKADKEWKYQVYG 451

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=xlh
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-DB=GenEmbl -QFMT=fastp -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosom62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10614954 @CN 1.1 3731 @runat_19012005_171526_25178 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.*

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- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
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- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sv.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2334	100.0	1356	6	BD247864 Transgeni
2	2334	100.0	1356	6	AR193433 Sequence
3	2334	100.0	1356	6	AR430218 Sequence
4	2314	99.1	1605	6	E31785 Trichothece

5	2314	99.1	1605	8	AB000874	AB000874	Gibberell
6	2314	99.1	3003	8	AB009607	AB009607	Gibberell
7	2314	99.1	8646	8	AB011417	AB011417	Gibberell
8	2296	98.4	1336	8	AF212605	AF212605	Gibberell
9	2296	98.4	1336	8	AF212608	AF212608	Gibberell
10	2291	98.2	1336	8	AF212602	AF212602	Gibberell
11	2291	98.2	1336	8	AF212603	AF212603	Gibberell
12	2291	98.2	1336	8	AF212604	AF212604	Gibberell
13	2291	98.2	1336	8	AF212606	AF212606	Gibberell
14	2287	98.0	1329	8	AY452807	AY452807	Gibberell
15	2287	98.0	1329	8	AY452808	AY452808	Gibberell
16	2286	97.9	1336	8	AF212607	AF212607	Gibberell
17	2277	97.6	1336	8	AF212582	AF212582	Gibberell
18	2277	97.6	1336	8	AF212583	AF212583	Gibberell
19	2277	97.6	1336	8	AF212584	AF212584	Gibberell
20	2277	97.6	1336	8	AF212594	AF212594	Gibberell
21	2277	97.6	1336	8	AF212601	AF212601	Gibberell
22	2276	97.5	1336	8	AF212595	AF212595	Gibberell
23	2276	97.5	1336	8	AF212597	AF212597	Gibberell
24	2276	97.5	1336	8	AF212598	AF212598	Gibberell
25	2276	97.5	1336	8	AF212599	AF212599	Gibberell
26	2276	97.5	1336	8	AF212600	AF212600	Gibberell
27	2273	97.4	1336	8	AF212596	AF212596	Gibberell
28	2272	97.3	1336	8	AF212585	AF212585	Gibberell
29	2272	97.3	1336	8	AF212587	AF212587	Gibberell
30	2272	97.3	1336	8	AF212588	AF212588	Gibberell
31	2271	97.3	1336	8	AF212589	AF212589	Gibberell
32	2271	97.3	1336	8	AF212612	AF212612	Fusarium
33	2265	97.0	1336	8	AF212613	AF212613	Fusarium
34	2265	97.0	1326	8	AY452813	AY452813	Fusarium
35	2262	96.9	1326	8	AY452814	AY452814	Fusarium
36	2257	96.7	1336	8	AF212614	AF212614	Fusarium
37	2257	96.7	1336	8	AF212611	AF212611	Fusarium
38	2255	96.6	1326	8	AY452810	AY452810	Fusarium
39	2254	96.6	1326	8	AY452811	AY452811	Fusarium
40	2254	96.6	1326	8	AY452812	AY452812	Fusarium
41	2247	96.3	1336	8	AF212609	AF212609	Fusarium
42	2247	96.3	1336	8	AF212610	AF212610	Fusarium
43	2244	96.1	1322	8	AY222642	AY222642	Gibberell
44	2244	96.1	1322	8	AY225882	AY225882	Gibberell
45	2244	96.1	1322	8	AY225882	AY225882	Gibberell

ALIGNMENTS

RESULT 1	BD247864	1356 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD247864				
DEFINITION	Transgenic plant and methods.				
ACCESSION	BD247864				
VERSION	BD247864.1				
KEYWORDS	JP 2002540787-A/4.				
SOURCE	Gibberella zeae				
ORGANISM	Gibberella zeae				
REFERENCE	1 (bases 1 to 1356)				
AUTHORS	Hohn,T.M., Peters,C., Salmeron,J.M., Janet, Reed,N. and Dawson,J.L.				
TITLE	Hypocromycetidae; Hypocreales; Nectriaceae; Gibberella.				
JOURNAL	Transgenic plant and methods				
COMMENT	Patent: JP 2002540787-A 4 03-DEC-2002; SYNGENTA PARTICIPATIONS AG OS Fusarium graminearum PN JP 2002540787-A/4 PD 03-DEC-2002 PF 29-MAR-2000 JP 2000609553 PR 31-MAR-1999 US 09/282995,11-FEB-2000 US 09/502852 PI THOMAS M HOHN, CHERYL PETERS, JOHN MANUEL SALMERON, JANET PI N REED, JOHN L DAWSON PC C12N15/09, A01H5/00, C12N1/15, C12N5/10, C12N1/15, C12R1/645, PC (C12N5/10, C12R1/91), C12N15/00, C12N5/00, C12N5/00, C12N5/00, C12R1/91) CC Transgenic plant and methods FH Key Location/Qualifiers FT source 1. .1356				

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FT /organism='Fusarium graminearum'.
source Location/Qualifiers
1. .1356
/organism="Gibberella zeae"
/mol_type="genomic DNA"
/db_xref="taxon:5518"

ORIGIN
Alignment Scores:
Pred. No.: 3 42e-167 Length: 1356
Score: 2334.00 Matches: 451
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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QY 101 MetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLys 120
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DB 481 ATGGTAGGCCAAGATGGGTGATCCGCTACTCTCCAGCGGTCGCTAACGCCCATTC 540
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DB 541 ACCGAGAGGAATGATCGGCCCATGAACCTCGATCGCAAGACGATAGTTCTTACCTTGA 600
QY 201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly 220
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QY 221 AspAlaValLeuThrProValSerAlaSerTyrAlaPhePheThrPheSerProLysAla 240
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QY 241 MetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSer 260
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QY 261 ThrAspAlaLeuSerAlaPheIleTyrLysSerAlaSerArgValArgLeuGluArg 280
DB 781 ACTGACGATGCTCTTCGCGGTTTCATCTGGAATCGGCCCTCTCGCGTGTCTCGAAGA 840

281 IleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGly 300
DB 841 ATCGATGGCTCTGCACCTACCGAGTCTGCCGTGCTGTGATGTCGACCGCAATGGT 900
QY 301 ValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGly 320
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QY 441 LysGluTyrThrLysTyrAlaGlnTyrValGly 451
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DEFINITION Sequence 5 from patent US 6346655.
ACCESSION AR193433
VERSION AR193433.1 GI:20239398
KEYWORDS Trichothecene-Resistant transgenic plants
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1356)
AUTHORS Hohn,T.M., Peters,C. and Salmeron,J.
TITLE Trichothecene-Resistant transgenic plants
JOURNAL Patent: US 6346655-A 5 12-FEB-2002;
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Location/Qualifiers
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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QY 21 ThrGlnIleSerLeuLeuTyrProValSerAspSerGlnTyrProThrIleValSer 40
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Qy 201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGly 220
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Db 1321 AAGGAGTGGACCAAGTATGCGCAGTACGTTGCT 1353
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DEFINITION Sequence 5 from patent US 6646184.
ACCESSION AR430218
VERSION AR430218.1 GI:40190948
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1356)
AUTHORS Hohn,T.M., Peters,C. and Salmeron,J.
TITLE Trichothecene-resistant transgenic plants
JOURNAL Patent: US 6646184-A 5 11-NOV-2003;
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source 1. 1356
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Score: 2334.00 Matches: 451
Percent Similarity: 100.00% Conservative: 0
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 DEFINITION Trichothecene 3-O-acetyltransferase gene.
 ACCESSION E31785
 VERSION E31785.1 GI:13018619
 KEYWORDS JP 2000032985-A/1.
 SOURCE Gibberella zeae
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE

1 (bases 1 to 1605)

Isamu, Y., Makoto, K., Akira, T., Hiroyuki, K. and Katsumi, Y.

Trichothecene 3-O-acetyltransferase gene

Patent: JP 2000032985-A 1 02-FEB-2000;

RIKAGAKU KENKYUSHO, ISAMU YAMAGUCHI

OS Fusarium graminearum

PD JP 2000032985-A/1

PN 02-FEB-2000

PP 15-JUL-1998 JP 1998200280

PR ISAMU YAMAGUCHI, MAKOTO KIMURA, AKIRA TAKATSUKI, HIROYUKI

KOSHINO, PI KATSUMI YONEYAMA

PC C12N15/09, A01H5/00, A01N63/00, C12N1/21, C12N5/10, C12N9/10// PC

(C12N15/09, C12R1/77), (C12N1/21, C12R1/19), (C12N5/10, C12R1/91), PC

C12N15/00,

PC C12N5/00, C12N15/00, C12R1/77), (C12N5/00, C12R1/91) CC

FH Key Location/Qualifiers

FT CDS 135..1487.

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source

1..1605

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Score: 2314.00 Matches: 447

Percent Similarity: 99.11% Conservatives: 0

Best Local Similarity: 99.11% Mismatches: 4

Query Match: 99.14% Indels: 0

DB: 6 Gaps: 0

US-10-614-954-6 (1-451) x E31785 (1-1605)

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Qy 41 ThrPheGluGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnVal 60

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RESULT 5

AB000874

LOCUS

DEFINITION

AB000874

AB000874.1 GI:2804249

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

98104153
9430709
2 (bases 1 to 1605)
Kimura,M.
Direct Submission
Submitted (04-FEB-1997) Makoto Kimura, The Institute of Physical
and Chemical Research (RIKEN), Microbial Toxicology Laboratory;
Hiroseawa 2-1, Wako, Saitama 351-01, Japan
(E-mail:mkimura@postman.riken.go.jp, Tel:81-048-467-9518,
Fax:81-048-462-4676)

FEATURES
source

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gene

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CDS

135. 1490

ORIGIN

Alignment Scores:
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Percent Similarity: 99.11% Conservative: 0
Best Local Similarity: 99.11% Mismatches: 4
Query Match: 99.14% Indels: 0
DB: 8 Gaps: 0

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DEFINITION 3-O-acetyltransferase, partial and complete cds.
ACCESSION AB009607
VERSION AB009607.1 GI:3252781
KEYWORDS Tril01; trichothecene 3-O-acetyltransferase; UTP-ammonia ligase.
SOURCE Gibberella zeae
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AUTHORS Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
TITLE Kimura,M., Shingu,Y., Yoneyama,K. and Yamaguchi,I.
JOURNAL Features of Tril01, the trichothecene 3-O-acetyltransferase gene,
MEDLINE related to the self-defense mechanism in Fusarium graminearum
PUBMED Biosci. Biotechnol. Biochem. 62 (5), 1033-1036 (1998)
REFERENCE 98312047
PUBMED 9648241
AUTHORS 2 (bases 1 to 3003)
TITLE Direct Submission
JOURNAL Submitted (06-DEC-1997) Makoto Kimura, The Institute of Physical
and Chemical Research (RIKEN), Microbial Toxicology Laboratory;
Hirosawa 2-1, Wako, Saitama 351-0198, Japan
(E-mail:mkimura@postman.riken.go.jp, Tel.81-48-467-9518,
Fax:81-48-462-4676)
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RESULT 7
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UTP-ammonia ligase and phosphate permease, complete cds.
ACCESSION
AB011417.1 GI:3724288
VERSION
3-O-acetyltransferase.
KEYWORDS
Gibberella zeae
SOURCE
Gibberella zeae
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE
1 (sites)
Kimura,M., Matsumoto,G., Shingu,Y., Yoneyama,K. and Yamaguchi,I.
The mystery of the trichothecene 3-O-acetyltransferase gene.
Analysis of the region around Tri101 and characterization of its
homologue from Fusarium sporotrichioides
FEBS Lett. 435 (2-3), 163-168 (1998)
JOURNAL
MEDLINE
98433864
PUBMED
9762900
REFERENCE
2 (bases 1 to 8646)
Kimura,M.
Direct Submission
Submitted (23-FEB-1998) Makoto Kimura, The Institute of Physical
and Chemical Research (RIKEN), Microbial Toxicology Laboratory;
Hirotsawa 2-1, Wako, Saitama 351-0198, Japan
(E-mail:mkimura@postman.riken.go.jp, Tel:81-48-467-9518,
Fax:81-48-462-4676)
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ORIGIN

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US-10-614-954-6 (1-451) x AB011417 (1-8646)

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DB 4836 AAGGAGTGCACCAAGTATGCGCAGTACGTTGTTGT 4868

RESULT 8

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AF212605
VERSION
AF212605.1
KEYWORDS
GI:12003706
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Gibberella zeae
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE
1 (bases 1 to 1336)

AF212605 1336 bp DNA linear PLN 26-JUN-2001

AUTHORS O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
 TITLE Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of *Fusarium graminearum*, the fungus causing wheat scab
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
 MEDLINE 20345085
 PUBMED 10869425
 REFERENCE 2 (bases 1 to 1336)
 AUTHORS O'Donnell, K.
 TITLE Direct Submission
 JOURNAL Submitted (08-DEC-1999) Microbial Properties Research, NCAR-ARS-USA, 1915 N. University St., Peoria, IL 61604, USA
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 Score: 2296.00 Matches: 444
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.37% Indels: 0
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 DB 3 ATGGCTTTCAAGATACAGCTCGACACCTCGGCCAGCTACCGGCTCTCTTCGATCTAC 62
 QY 21 ThrGlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSer 40
 DB 63 ACCCAATCAGTCTCTACCCGCTCTGATTCCTCAATATCCCACTATTGTGAGC 122
 QY 41 ThrPheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnVal 60
 DB 123 ACCTTCGAGCAGGTCTTAAGCGCTTCCTCGAAGCGGTCCTCCATGGTCCGAGGCCAGGTC 182
 QY 61 LysAlaGluGlyLeuSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp 80
 DB 183 AAGCCGAGGCGATTAGCGGGAACACAGGAACCTTCCTTATCGTCCCTTTTGGAGAC 242
 QY 81 ValProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGly 100
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 QY 161 MetValGlyGlnAspAlaValIleArgLeuSerLysAlaCysArgAsnAspProPhe 180
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 QY 261 ThrAspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArg 280
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 QY 281 IleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGly 300
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 QY 301 ValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGly 320
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 QY 421 GlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAsp 440
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 AF212608 1336 bp DNA linear PLN 26-JUN-2001
 LOCUS Gibberella zeae strain NRRL29169 trichothecene
 DEFINITION 3-O-acetyltransferase, partial cds.
 ACCESSION AF212608
 VERSION AF212608.1 GI:12003712
 KEYWORDS Gibberella zeae

ORGANISM	Gibberella zeae	121	ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGln	140
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.	Db		422
AUTHORS	1 (bases 1 to 1336)	QY		160
TITLE	O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H. Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of <i>Fusarium graminearum</i> , the fungus causing wheat scab	Db		482
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)	QY		180
MEDLINE	20345085	Db		542
PUBMED	10869425	QY		200
REFERENCE	2 (bases 1 to 1336)	Db		602
AUTHORS	O'Donnell, K.	QY		220
TITLE	Direct Submission	Db		662
JOURNAL	Submitted (08-DEC-1999) Microbial Properties Research, NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA	QY		722
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ORIGIN		QY		1622
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81 ValProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGly	100	Db		2642
243 GTTCTCGTGTGTAGTGAAGACCTCCGCGATGATCTCTTACGCCGCCACGATCGAGGT	302	QY		2702
101 MetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLys	120	Db		2762
303 ATGAGNAAGCCGGGATACCTTATGGCGATGTTTGACGAGAACATCATTCGCCCAAGGAG	362	QY		2822
121 ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGln	140	Db		2882
363 ACCTTACCTATTGGACCTGCTGCTCCGACGACCAAGCTGTAATCTTATTGCGAG	422	QY		2942
141 LeuAsnPheIleLysGlyGlyLeuLeuThrValAsnGlyGlnHisGlyAlaMetAsp	160	Db		3002
423 CTCACCTTATCAAGGCGGACTCATCTCTCAACGACGACGACGCTGCTATGGAT	482	QY		3062
161 MetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPhe	180	Db		3122
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221 AspAlaValLeuThrProValSerAlaSerTyrAlaPhePheThrPheSerProLysAla	240	Db		3482
663 GACGCTGTTCTCACGCCGTCAGTCAAGCTGGCGGTCTTCAATTCAGCCCCAAGGCC	722	QY		3542
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783 ACTGACGATGCTCTTTGGCGTTCATCTGGAATCGGCTCTCGGTGCTCTCGAAGA	842	QY		3782
281 IleAspGlySerAlaProThrCluPheCysArgAlaValAspAlaArgProAlaMetGly	300	Db		3842
843 ATCGATGGCTTCGACCTACCGAGTCTCGCGTCTGTTGATGCTCGACCGGCAATGGT	902	QY		3902
301 ValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGly	320	Db		3962
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963 GAAATCGCCCAACGAGTCACTCGCGCAACAGCATCACGCTCTCGTTCGAACTCGAC	1022	QY		4142
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361 SerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTyr	380	Db		4322
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1143 GCCAAGGTGGGACTCTGGGATTTACGACTTGGGCTCGGACTGGTAAGCCGAGACTGTG	1202	QY		4502
401 ArgArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAsp	420	Db		4562
1203 AGACGCCCACTTTGAGCCTGTTGAGCTTGATGTACTTTATGCCCCAGAGGCTGAT	1262	QY		4622
421 GlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAsp	440	Db		4682
1263 GCGGAGTTCTGTGCGCGCTTCTCTGAGGGATGAGGATATGACCGGATTTGAAGCGGAT	1322	QY		4742
441 LysGluTyrThr	444	Db		4802
1323 AAGGAGTGAC	1334	QY		4862
RESULT 10		Db		4922
AF212602	1336 bp	QY		4982
LOCUS	AF212602	Db		5042
DEFINITION	Gibberella zeae strain NRRL5883 trichothecene 3-O-acetyltransferase, partial cds.	QY		5102

ACCESSION	AF212602	AF212602.1	GI:12003700	QY	101	MetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLys	120
VERSION	AF212602.1	GI:12003700		DB	303	ATGAGAAAGCGGGATACCTATGGCGATGTTGACGAGAACATCATCGCGCAAGAAAG	362
KEYWORDS							
SOURCE	Gibberella zeae			QY	121	ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGln	140
ORGANISM	Gibberella zeae			DB	363	AGTTACCTATTGGACCTGGTACTGGTCCGACGACCCCAAGCGCTGAATCTTATTGCAG	422
REFERENCE	1 (bases 1 to 1336)			QY	141	LeuAsnPheIleGlyGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAsp	160
AUTHORS	O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.			DB	423	CTCAACTTCATCAAGGGCGGACTCATCTCTCACTGTCAAGCGACGACGCTGTATGGAT	482
TITLE	Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of <i>Fusarium graminearum</i> , the fungus causing wheat scab			QY	161	MetValGlyGlnAspAlaValIleArgLeuSerLysAlaCysArgAsnAspProPhe	180
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)			DB	483	ATGGTAGGCCAAGATCGGTGATCCGTCTTCCAGCGCGCGTACGACCCCATTC	542
MEDLINE	20345085			QY	181	ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGlu	200
PUBMED	10869425			DB	543	ACCGAAGAGGAATGACGGCCATGACCTCGATCGCAAGACGATAGTTCCTTACCTTGA	602
REFERENCE	2 (bases 1 to 1336)			QY	201	AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly	220
AUTHORS	O'Donnell, K.			DB	603	AACTATACGATTGGCCCGGAGGTAGATCATCATGATGTCAAACCTGATGTAGTGGT	662
TITLE	Direct Submission			QY	221	AspAlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAla	240
JOURNAL	Submitted (08-DEC-1999) Microbial Properties Research, NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA			DB	663	GACGCTGTCTCACGCCGTCAGTGCAGCTGGCGCTTCTTCACATTCAGCCCCAGGCC	722
FEATURES	Location/Qualifiers			QY	241	MetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSer	260
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	RLEIDGSAFTFCFADVPAMGVSNNTYFGLQNMTHNSTGTEIANESLGTASRL			QY	421	GlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAsp	440
	RSELDPASMRQTRGLATYLHNHPDKSNVSLTADADPSTVMLSSWAKVLWDYDFGL			DB	1263	GGCGAGTTCTGTGCGCGCTTCTCTGAGGATGAGGATATGACCGATTTGAAGCGCGAT	1322
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Alignment Scores:							
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US-10-614-954-6 (1-451) x AF212602 (1-1336)							
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DB	63	ACCAATATGATCTCTTACCCCGCTCTGATTCCTCTCAATATCCACTATTGTGACG	122				
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DB	123	ACCTTCGAGCAAGGTCTTAAGCGCTTCTCCGAAGCGCTCCATGGGTGCGAGGCCAGGTC	182				
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DB	183	AAAGCCGAGGCGATTACGAGGGGAAACACAGGAACCTCTCTTATCGTCCCTTTGAGGAC	242				
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AF212603 1336 bp DNA linear PLN 26-JUN-2001
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 DEFINITION 3-O-acetyltransferase, partial cds.
 ACCESSION AF212603
 VERSION AF212603.1 GI:12003702
 KEYWORDS
 SOURCE Gibberella zeae
 ORGANISM Gibberella zeae
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypotrachales; Nectriaceae; Gibberella.
 1 (bases 1 to 1336)
 O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
 Gene genealogies reveal global phylogeographic structure and
 TITLE reproductive isolation among lineages of *Fusarium graminearum*, the
 fungus causing wheat scab
 Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
 JOURNAL 20345085
 MEDLINE 10869425
 PUBMED
 REFERENCE 2 (bases 1 to 1336)
 O'Donnell, K.
 Direct Submission
 TITLE Submitted (08-DEC-1999) Microbial Properties Research,
 JOURNAL NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
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 Best Local Similarity: 99.77% Mismatches: 1
 Query Match: 98.16% Indels: 0
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 US-10-614-954-6 (1-451) x AF212603 (1-1336)

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3-O-acetyltransferase, partial cds.
ACCESSION
AF212604
VERSION
AF212604.1 GI:12003704
KEYWORDS
SOURCE
Gibberella zeae
ORGANISM
Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE
1 (bases 1 to 1336)
O'Donnell, K., Kistler, H.C., Tacke, B.K. and Caspar, H.H.
AUTHORS
Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of Fusarium graminearum, the
fungus causing wheat scab
TITLE
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
JOURNAL
MEDLINE
20345085
PUBMED
10869425
REFERENCE
2 (bases 1 to 1336)
O'Donnell, K.
AUTHORS
Direct Submission
TITLE
Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
JOURNAL
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Query Match: 98.16% Indels: 0
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 VERSION AF212606.1 GI:12003708
 KEYWORDS Gibberella zeae
 SOURCE Gibberella zeae
 ORGANISM Gibberella zeae

REFERENCE 1 (bases 1 to 1336)
 AUTHORS O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
 TITLE Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of *Fusarium graminearum*, the fungus causing wheat scab

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
 MEDLINE 20345085
 PUBMED 10869425
 REFERENCE 2 (bases 1 to 1336)
 AUTHORS O'Donnell, K.
 DIRECT SUBMISSION
 TITLE Submitted (08-DEC-1999) Microbial Properties Research,
 JOURNAL NCAUR-ARS-USA, 1815 N. University St., Peoria, IL 61604, USA

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ORIGIN

Alignment Scores:
 Pred. No.: 5,96e-164 Length: 1336
 Score: 2291.00 Matches: 443
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US-10-614-954-6 (1-451) x AF212606 (1-1336)

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VERSION   1
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Hypocryomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1. (bases 1 to 1329)
AUTHORS   O'Donnell, K., Ward, T.J., Geiser, D.M., Corby Kistler, H. and Aoki, T.
TITLE      Genealogical concordance between the mating type locus and seven
other nuclear genes supports formal recognition of nine
phylogenetically distinct species within the Fusarium graminearum
clade
JOURNAL   Fungal Genet. Biol. 41 (6), 600-623 (2004)
PUBMED    15121083
REFERENCE 2 (bases 1 to 1329)
AUTHORS   O'Donnell, K.
TITLE      Direct Submission
JOURNAL   Submitted (29-OCT-2003) Microbial Genomics, USDA, ARS, 1815 N.
University St., Peoria, IL 61604, USA
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US-10-614-954-6 (1-451) x AY452807 (1-1329)

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363 ValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAlaLys 382
1082 GTATCCTTACCGGCTGATCGGACCCCATCTACAGCGTCTATGCTGAGTCTTTGGGCAAG 1141

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QY	363	ValSerLeuThrAlaAlaAspProSerThrSerValMetLeuSerSerTrpAlaLys	382
Db	1082	GTATCCCTGACGGCTGATCGGACCCATCTACGAGCTCATGCTGAGTTCTTGGGCAAAG	1141
QY	383	ValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyProGluThrValArgArg	402
Db	1142	GTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGTAAGCCCGAGACTGTGAGACGG	1201
QY	403	ProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGlyGlu	422
Db	1202	CCAATCTTTGAGCCTGTTGAGAGCTTGATGTACTTTATGCCCPAGAGGCTGATGGCGAG	1261
QY	423	PheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLysGlu	442
Db	1262	TTCTGTGCGGCGCTTTCTCTGAGGGATGAGGATATGGACCGATTGAAGGGGATAGGAG	1321
QY	443	TrpThr	444
Db	1322	TGGACC	1327

Search completed: January 24, 2005, 07:55:16
Job time : 6092 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 23, 2005, 20:29:16 ; Search time 676 Seconds
(without alignments)
3502.202 Million cell updates/sec

Title: US-10-614-954-6
Perfect score: 2334
Sequence: 1 MAFKIQDLTGLQPLGLSIY.....EDMDRLKADKEWTKYAYVG 451

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODEL=frame+ p2n.model -DEV=xlh
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3: Geneseqn2000s: *
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10: Geneseqn2003cs: *
11: Geneseqn2003ds: *
12: Geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2334	100.0	1356	3	AA54209 Sequence
2	2334	100.0	1356	12	Adn37285 Trichothene
3	2314	99.1	1605	3	Aaz89368 F. gramin
4	1860.5	79.7	1403	3	AA54206 Sequence
5	1860.5	79.7	12949	3	AA54213 Transform
6	1860.5	79.7	13737	3	AA54212 Transform

7	962.5	41.2	1425	3	AA54210	AA54210 Sequence
8	445.5	19.1	695	3	AAFI2071	Aafi2071 Aspergill
9	356.5	15.3	1440	10	ADE81194	Ad81194 Orfil cod
10	356.5	15.3	72149	10	ADE81173	Ad81173 ML-2368 s
11	351	15.0	482	8	AB254817	Ab254817 Aspergill
12	175	7.5	1508	12	ADO70366	Ado70366 Barley ag
13	170.5	7.3	1587	10	ABX78350	Abx78350 Wheat str
14	170.5	7.3	1596	3	AAC38228	Aac38228 Arabidops
15	169.5	7.2	1593	3	AAC49441	Aac49441 Arabidops
16	168.5	7.2	1735	10	ABX78344	Abx78344 Corn stre
17	166.5	7.1	1455	8	ADA70751	Ada70751 Rice gene
18	165.5	7.1	1207	12	ADO70371	Ado70371 Barley ag
19	161	6.9	1556	10	ABX78348	Abx78348 Soybean s
20	158.5	6.8	1241	12	ADO70384	Ado70384 Barley ag
21	157.5	6.7	1220	12	ADO70368	Ado70368 Wheat par
22	154.5	6.6	1296	3	AAC64783	Aac64783 Mango alc
23	154	6.6	1471	3	AAC40295	Aac40295 Arabidops
24	151.5	6.5	1605	2	AAT37310	Aat37310 Aromatic
25	143	6.1	1428	6	AB213585	Ab213585 Arabidops
26	143	6.1	1428	6	ADG88181	Adg88181 A. thalia
27	143	6.1	1428	6	ADG87834	Adg87834 A. thalia
28	143	6.1	1428	8	ADA68064	Ada68064 Arabidops
29	143	6.1	1428	12	ADN72452	Adn72452 Thale cre
30	143	6.1	1551	3	AAC48784	Aac48784 Arabidops
31	142.5	6.1	1329	3	AAC45418	Aac45418 Arabidops
32	142.5	6.1	1471	3	AAC45423	Aac45423 Arabidops
33	142	6.1	1347	5	AAD03360	Aad03360 Taxus cus
34	142	6.1	1347	10	ADB91966	Adb91966 Acyltrane
35	141.5	6.1	1452	8	ADA69994	Ada69994 Rice gene
36	139.5	6.0	1815	3	AAC48422	Aac48422 Arabidops
37	139.5	6.0	3499	6	AAD41127	Aad41127 Arabidops
38	139.5	6.0	7438	6	AAD41126	Aad41126 Arabidops
39	135	5.8	1542	2	AAQ54685	Aaq54685 Anther sp
40	134.5	5.8	1477	3	AAC39128	Aac39128 Arabidops
41	134	5.7	3706	2	AAQ54693	Aaq54693 Anther sp
42	134	5.7	3706	2	AAQ58340	Aaq58340 Tobacco A
43	132.5	5.7	1125	3	AAC40902	Aac40902 Arabidops
44	132.5	5.7	83698	6	ABN85767	Abn85767 Arabidops
45	132	5.7	1317	5	AAD03346	Aad03346 Taxus cus

ALIGNMENTS

RESULT 1
AAA54209 standard; DNA; 1356 BP.
XX
AC AAA54209;
XX
DT 15-SEP-2003 (revised)
DT 26-FEB-2001 (first entry)

Sequence encoding trichothecene resistance polypeptide.

Trichothecene resistance; resistant; crop protection; mycotoxin; fungus;
wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;
ds.

Gibberella zeae.

Key Location/Qualifiers
CDS 1..1356
FT /tag=a
FT /product="Trichothecene resistance polypeptide"

XX WO2000060061-A2.

PD 12-OCT-2000.

XX 29-MAR-2000; 2000WO-EP002769.

XX 31-MAR-1999; 99US-00282995.

PR 11-FEB-2000; 2000US-00502852.

XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GRS MBH.
XX
PI Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;
XX
DR WPI; 2000-679374/66.
DR P-PSDB; AAB03935.
XX
PT Plant cell for preventing mycotoxin contamination of wheat, maize, barley
PT or rice plant, comprises heterologous polynucleotide encoding gene
PT product expressed in cell, having trichothecene resistance activity.
XX
PS Claim 8; Page 48-49; 62pp; English.
FX
SS A heterologous gene encoding a gene product which confers trichothecene
CC resistance can be used to transform plant cells to make them resistant to
CC fungal infection. The transformation method is useful for preventing
CC mycotoxin contamination of a plant, particularly a crop plant such as
CC wheat, maize, barley or rice, and for reducing and/or preventing the
CC growth of a fungus of the genus *Fusarium* that produces a trichothecene,
CC preferably comprising a C-3 hydroxyl group, by growing transformed crop
CC plants in an area which is moderate to severe fungal infestation.
CC (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 1356 BP; 319 A; 385 C; 349 G; 303 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3 7e-219 Length: 1356
Score: 2334.00 Matches: 451
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-614-954-6 (1-451) x AA54209 (1-1356)

QY 1 MetAlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyr 20
Db 1 ATGGCTTTCAAGATACAGTTCGACACCTCGGCGAGTACCAGGCTCCTTTTCGATCTAC 60
QY 21 ThrGlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSer 40
Db 61 ACCCAATCAGTCTCTCTACCCCGCTCTGATTCCTCTCAATATCCCACTATTGTCAGC 120
QY 41 ThrPheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnVal 60
Db 121 ACCTTCGACAGGCTCTTAAGCGCTTCTCGAAGCGTCCCATGGGTCCGAGGCCAGGTC 180
QY 61 LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp 80
Db 181 AAAGCCGAGGCAATTAGCGAGGGAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGAC 240
QY 81 ValProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGly 100
Db 241 GTTCTCTGGTGTGTAGTGAAGACCTCCCGGATGATCCTTCAGCGCCACGATCGAGGT 300
QY 101 MetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLys 120
Db 301 ATGAGAAAGCGGGATACCTATGGCGATGTTTGACGAGAAATCATCATCGGCCAAGGAG 360
QY 121 ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGln 140
Db 361 ACGTTACCTATTGGACCTGTGTGTCGCGAGCAACCAAGCCTGTATTTCTATTTCGAC 420
QY 141 LeuAsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAsp 160
Db 421 CTCACCTTATCAGGGCGGAGCTATCTCTCATCTGTCAACGAGCAGCAGGTGCTATGAT 480
QY 161 MetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPhe 180
Db 481 ATGGTAGGCCAAGATGCGGTGATCCGTCTACTCTCCAGGCGTGCCTTAACGACCAATTC 540

QY 181 ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGlu 200
Db 541 ACCGAGAGGAAATGAGCGCCATGAACTTCGATCGCAACAGCATAGTTCTTACCTTGA 600
QY 201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly 220
Db 601 AACTATACGATTGGCCCGAGGTAGATCATCATGATTTGTCAAAGCTGATAGTGTGTGT 660
QY 221 AspAlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAla 240
Db 661 GACGCTGTTCTCAGCGCGGTGAGTGAAGCTGGCGTCTTTCACATTCAGCCCCAAGGCC 720
QY 241 MetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSer 260
Db 721 ATGTCCAGAGCTCAAGGATGCTCTACCAAGACTCTTGACGCATCAACAAGTTCTGTGTG 780
QY 261 ThrAspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArg 280
Db 781 ACTGACGATGCTCTTTTCGCGCTTCATCTGGAATCGGCTCTCGGTGCTCTCGAAAGA 840
QY 281 IleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGly 300
Db 841 ATCGATGGCTCTGACCTACCGAGTCTGCGGTGCTGTGTGATGCTCGACCGCAATGGT 900
QY 301 ValSerAsnAsnTyrProGlyLeuGlnAsnMetThrTyrHisAsnSerThrIleGly 320
Db 901 GTCTCGAACAACTACCCAGGCTTCTTCAAAACATGACCTACCACTCGACCATCGGC 960
QY 321 GluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspPro 340
Db 961 GAAATCGCCCAACGAGTCACTCGGCGCAACAGCATCACGCTTCGTTCAGAACTCGACCCC 1020
QY 341 AlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLys 360
Db 1021 GCGAGCATGGCGGACGACAGAGGTCTCGCGAGCTACTGTCACACACACCCGACAG 1080
QY 361 SerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrp 380
Db 1081 TCCAAAGTATCCTCGACGCTGATCGGACCCATCTACGAGGTCATGTGAGTCTTCTGGT 1140
QY 381 AlaLysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLysProGluThrVal 400
Db 1141 GCCAAGGTGGGACTCTGGGATTTACGACTTTGGGCTCGGAGTGGGTAAAGCCGAGACTGT 1200
QY 401 ArgArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAsp 420
Db 1201 AGACGCGCAATCTTTGAGCGCTTTCAGAGCTTGATGTACTTTATGCCCAAGAGCTGT 1260
QY 421 GlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAsp 440
Db 1261 GCGGAGTTCGTGTGCGCGCTTCTCTGAGGGATGAGGATATGGACCGGATTGAAGCGGAT 1320
QY 441 LysGluTyrThrLysTyrAlaGlnTyrValGly 451
Db 1321 AAGGAGTGGACCAAGTATGCGCAGTACGTTGT 1353

RESULT 2
ADN37285
ID ADN37285 standard; DNA; 1356 BP.
XX
AC ADN37285;
XX
DT 15-JUL-2004 (first entry)
DE Trichothecene 3-O-acetyltransferase encoding DNA SEQ ID NO:29.
XX maternal tissue; plant seed; plant;
KW bifunctional alpha-amylase subtilisin inhibitor gene promoter;
KW alpha-amylase inhibitor promoter; ASI promoter; plant protectant;
KW viricide; vaccine; resistance; infection; *Fusarium graminearum*;
KW trichothecene 3-O-acetyltransferase; enzyme; gene; ds.
OS *Gibberella zeae*.

XX	Key	Location/Qualifiers	QY	1	MetAlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyr	20
FT	CDS	1..1356	Db	1	ATGGCTTTCAAGATACAGCTCGACACCTCGGCCAGCTACACGGCTCTCTTCGATCTAC	60
FT		/tag= a				
FT		/product= "Trichothecene 3-O-acetyltransferase protein"				
XX	WO2004035790-A1.		QY	21	ThrGlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSer	40
XX	29-APR-2004.		Db	61	ACCAAATCAGTCTCTCTTACCCCGTCTCTGATCTCTCAATATATCCCACTATTGTGACG	120
XX	17-OCT-2003; 2003WO-AU001381.		QY	41	ThrPheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnVal	60
XX	17-OCT-2002; 2002AU-00952143.		Db	121	ACCTTCGAGCAAGGCTTTAAGCGCTTCTCGAAGCGCTCCCATGGGTGCGCAGCCAGGTC	180
XX	(MOLE-) MOLECULAR PLANT BREEDING NOMINEES LTD.		QY	61	LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp	80
PA	(GRAI-) GRAINS RES & DEV CORP.		Db	181	AAAGCCGAGGGCATTTAGCGAGGGAACACAGGAACCTCTCTTATCGTCCCTTTTGGAGAC	240
XX	Furtado A, Henry RJ;		QY	81	ValProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGly	100
XX	WPI; 2004-348462/32.		Db	241	GTTCCTCGGTGTGTAGTGAAGACCTCCGCGATGATCTTCAGCGCCCAAGATCGAGGT	300
XX	P-PSDB; ADN37286.		QY	101	MetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLys	120
XX	Expressing nucleic acid or protein in a plant seed, useful in enhancing		Db	301	ATGAGAAAGCGGGATACCTATGGCGATGTTTGACGAGAACATCATCGCGCCCAAGGAG	360
PT	resistance of a plant against Fusarium graminearum and barley stripe		QY	121	ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGln	140
PT	mosaic virus, comprises expressing a bifunctional alpha-amylase		Db	361	ACGTTACCTATTGGACCTGGTACTGGTCCGACGACCCCAAGCCTGTAATCTTATTGCGAG	420
PT	subtilisin inhibitor promoter.		QY	141	LeuAsnPheIleLysGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAsp	160
PS	Claim 20; SEQ ID NO 29; 169pp; English.		Db	421	CTCAACTTCATCAAGGGCGGACTCATCTCTCAAGCGTGGCGTAAAGCTGCTATGGAT	480
CC	The present invention describes a method for expressing nucleic acid or		QY	161	MetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPhe	180
CC	protein in the maternal tissue of a plant seed. The method comprises		Db	481	ATGGTAGGCCAAGATGGGTGATCGGTCTCTCAAGCGTGGCGTAAAGCTGCTATGGAT	540
CC	expressing isolated nucleic acid operably under the control of a		QY	181	ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProThrLeuGlu	200
CC	bifunctional alpha-amylase subtilisin inhibitor (ASI) gene promoter that		Db	541	ACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAGACGATAGTCTTCTTACCTTGAA	600
CC	is operable in the maternal tissue. Also described: (1) a method of		QY	201	AsnThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly	220
CC	enhancing or conferring resistance of a plant against: (a) Fusarium		Db	601	AACTATACGATTGGCCCGGAGGTAGATCATCATGATGTCAAAGCTGATAGTGGTGGT	660
CC	graminearum (head scab); and (b) barley stripe mosaic virus (BSMV); (2)		QY	221	AspAlaValLeuThrProValSerAlaSerTrpAlaPheThrPheSerProLysAla	240
CC	an isolated transformed wheat and barley seed that expresses isolated		Db	661	GAACGTGTTCTCACGCCGCTCAGTGCAGCTGGCGGTCTTTCACATTCAGCCCAAGGCC	720
CC	nucleic acid encoding respectively a plant defence protein and a BSMV		QY	241	MetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSer	260
CC	coat protein or an inhibitory RNA that prevents, inhibits or reduces		Db	721	ATGTCAGAGCTCAAGGATGCTGCTACCAAGACTCTTGACGCATCAACAAAGTTCTGTGTCG	780
CC	expression of a BSMV movement protein placed operably under the control		QY	261	ThrAspAspAlaLeuSerAlaPheIleThrLysSerAlaSerArgValArgLeuGluArg	280
CC	of the ASI gene promoter where the seed exhibits enhanced resistance		Db	781	ACTGACGATGCTCTTTCGCGGTTCATCTGGAATCGCCCTCTCGCGTGGTCTCGAAGA	840
CC	against Fusarium graminearum (head scab) and BSMV by virtue of the		QY	281	IleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGly	300
CC	presence of the nucleic acid compared to an otherwise isogenic line that		Db	841	ATCGATGGCTCTGCACCTACCGAGTTCTGCCGTGCTGTGTGATGCTCGACCGCAATGGGT	900
CC	does not express the nucleic acid placed operably under the control of		QY	301	ValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGly	320
CC	the ASI gene promoter; (3) a method of producing an immunogenic		Db	901	GTCTCGAACCAACTACCCAGGCTTCTTCAAAACATGACCTACCAACCTCGACCATCGGC	960
CC	tissue of a plant seed produced by a process that comprises performing		QY	321	GluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspPro	340
CC	the method of (1); (5) a method of enhancing the nutritional quality of		Db	961	GAATCGCCCAACGAGTCACTCGCGCAACAGCATCAACGCTTCTGTTTCAAGAACTCGACCC	1020
CC	bran or animal fodder; and (6) an isolated bran or maternal tissue of a		QY	341	AlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLys	360
CC	seed produced by a process that comprises performing the method of (5).		Db	1021	GCAGCATCGCGCAGCAACAGAGGTCTCGCGAGTACTCGCACCAACACCCCGACAG	1080
CC	The composition has plant protectant and virucide activities, and can be					
CC	used in vaccines. The method is useful in expressing nucleic acid or					
CC	protein in the maternal tissue of a plant seed. The method and ASI gene					
CC	promoter are useful in enhancing or conferring resistance of a plant					
CC	against Fusarium graminearum and BSMV and in enhancing the nutritional					
CC	quality of bran or animal fodder. The seed or bran product and					
CC	composition are useful as an oral vaccine against infection in the					
CC	gastrointestinal, respiratory and urogenital tracts. The present sequence					
CC	encodes the Fusarium graminearum (Gibberella zeae) trichothecene 3-O-					
CC	acetyltransferase, which is used in the exemplification of the present					
CC	invention.					
XX	Sequence 1356 BP; 319 A; 385 C; 349 G; 303 T; 0 U; 0 Other;					

Alignment Scores:
 Pred. No.: 3,7e-219 Length: 1356
 Score: 2334.00 Matches: 451
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-10-614-954-6 (1-451) x ADN37285 (1-1356)

QY 361 SerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTyr 380
 Db 1081 TCCAACGTATCCCTGACGGCTGATGCGGACCCATCTACCAAGCTCATGCTGAGTTCTGG 1140
 QY 381 AlalyseValGlyLeuTyrAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrVal 400
 Db 1141 GCCAAGTGGGACTCTCGGATTACGACTTTGGGCTCGGACTGGGTAAAGCCGAGACTGTG 1200
 QY 401 ArgArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAsp 420
 Db 1201 AGACGGCCATCTTTGAGCCCTGTTGAGAGCTTGATGTACTTTATGCCAAGAGCTGAT 1260
 QY 421 GlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAsp 440
 Db 1261 GGGCAGTTCTGTGGCGGCTTTCTCTGAGGGATGAGGATATGACCGATTGAAGGGCGAT 1320
 QY 441 LysGluTyrThrLysTyrAlaGlnTyrValGly 451
 Db 1321 AAGAGTGGACCAAGTATGCCAGTACGTTGGT 1353

RESULT 3
 AAZ89368
 ID AAZ89368 standard; DNA; 1605 BP.
 AC AAZ89368;
 XX
 DT 15-SEP-2003 (revised)
 DT 09-JUN-2000 (first entry)
 XX
 DE F. graminearum trichothecene 3-O-acetyltransferase DNA.
 XX
 KW Trichothecene 3-O-acetyltransferase; selective marker; ds.
 XX
 OS Gibberella zeae.
 XX
 FH Location/Qualifiers
 FT CDS 135..1490
 FT /*tag= a
 FT /product= "trichothecin 3-O-acetyltransferase"
 XX
 PN JP2000032985-A.
 XX
 PD 02-FEB-2000.
 XX
 PF 15-JUL-1998; 98JP-00200280.
 XX
 PR 15-JUL-1998; 98JP-00200280.
 XX
 PA (RIKA) RIKAGAKU KENKUSHO.
 PA (YAMA/) YAMAGUCHI I.
 XX
 DR WPI; 2000-274037/24.
 DR P-PSDB; AAY51848.
 XX
 PT Trichothecin 3-O-acetyltransferase gene useful as a selective marker in
 PT gene manipulations in eukaryotic host cells.
 XX
 PS Claim 3; Page 16-18; 25pp; Japanese.
 XX
 CC This invention describes a novel protein with trichothecin 3-O-
 CC acetyltransferase activity. The gene is used as a selective marker in a
 CC gene manipulation using eukaryote as the host cell. This sequence encodes
 CC the trichothecin 3-O-acetyltransferase isolated from *Fusarium*
 CC *graminearum*. (Updated on 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 1605 BP; 397 A; 459 C; 393 G; 356 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,32e-217 Length: 1605
 Score: 2314.00 Matches: 447
 Percent Similarity: 99.11% Conservative: 0
 Best Local Similarity: 99.11% Mismatches: 4
 Query Match: 99.14% Indels: 0

DB: 3 Gaps: 0

US-10-614-954-6 (1-451) x AAZ89368 (1-1605)

QY 1 MetAlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyr 20
 Db 135 ATGGCTTTTCAAGATACAGCTCGACACCCCTCGGCGAGCTACCAAGGCTCTCTTCGATCTAC 194
 QY 21 ThrGlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSer 40
 Db 195 ACCCAATCAGTCTCTCTACCCCGCTCTGATCCCTCTCAATATCCCACTATTGTGCAG 254
 QY 41 ThrPheGluGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnVal 60
 Db 255 ACCTTCGACCAAGGCTTTAAGCGCTTCTCCGAAGCGCTCCCATGGTTCGAGGCCAGGTC 314
 QY 61 LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp 80
 Db 315 AAAGCCGAGGGCATTTAGCGAGGGAACAACGGGAACCTCTTATCGTCTCTTTTTCGAGGAC 374
 QY 81 ValProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGly 100
 Db 375 GTTCTCTGTTGTAGTGAAGACCTCCGCGATGATCCTTCAGCGCCACGATCGAGGGT 434
 QY 101 MetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLys 120
 Db 435 ATGAGAAAGGGCGGATACCTTATGGCGATGTTTTCGAGAGAACATCATCGCGCCAAAGGAG 494
 QY 121 ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuGln 140
 Db 495 ACCTTACCTATTGGACCTGGTACTGGCCCGACGACCCCAAGCCTGTGATTCTATTTCGAG 554
 QY 141 LeuAsnPheIleLysGlyGlyLeuLeuThrValAsnGlyGlnHisGlyAlaMetAsp 160
 Db 555 CTCAACTTCATCAAGGGGGGACTCATCTCACTGTCAACGACACACGCTGCTATGGAT 614
 QY 161 MetValGlyGlnAspAlaValIleArgLeuSerLysAlaCysArgAsnAspProPhe 180
 Db 615 ATGGTAGGCCAAGATGCGGTGATCGCTCTACTCTCAAGGCGTCCGTAACGACCATTC 674
 QY 181 ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGlu 200
 Db 675 ACCGAAGAGGAATGACGGCCATGAACCTCGATCCAAAGACAGATAGTTCCTTACCTTAA 734
 QY 201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly 220
 Db 735 AACTACAGATTGGCCCGGAGGTAGATCATCAGATTGTCAAACCTGATGTAGTGTGGT 794
 QY 221 AspAlaValLeuThrProValSerAlaSerTyrAlaPhePheThrPheSerProLysAla 240
 Db 795 GACGCTGTTCTCACGCCGCTCAGTCAAGCTGGGCGTTCTTCAAATTCAGCCCAAGGCC 854
 QY 241 MetSerGluLeuLysAspAlaThrLysThrLeuAspAlaSerThrLysPheValSer 260
 Db 855 ATGTCAAGAGCTCAAGAGTGTGCTTACCAAGACTCTTGACGCATCAACAAGTTCGTGTGG 914
 QY 261 ThrAspAspAlaLeuSerAlaPheIleTyrLysSerAlaSerArgValArgLeuGluArg 280
 Db 915 ACTGACGATGCTCTTTCGGCGTTTCATCTGGAATTCGGCTCTCGCGTGGCTCTCGAAGA 974
 QY 281 IleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGly 300
 Db 975 ATCGATGGCTCTGCAACCTTACCGAGTCTTCGCGCTGTGTGTGATGCTCGACCGCAATGGT 1034
 QY 301 ValSerAsnAsnTyrProGlyLeuGlnAsnMetThrTyrHisAsnSerThrIleGly 320
 Db 1035 GTCTGAAACAACCTCCCGAGGCTTCTTCAAACATGACCTACCACTCCACCATCCGC 1094
 QY 321 GluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspPro 340
 Db 1095 GAAATCGCAACGAGTCACTCGCGCAACACAGCATCAGCCCTTCGTTTCAGATCGACCCC 1154
 QY 341 AlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLys 360

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Db      1155 GCAGGATGCGCCAGGAAACAGAGTCTCGGACGTACCTGCACAAACCCCGCAAG 1214
QY      361 SerAsnValSerLeuThrAlaAspProSerThrSerValMetLeuSerSerTrp 380
Db      1215 TCCAAAGTATCTCTGACGGCTGATGGGACCCATCTACCAAGCTCATGCTGAGTCTTGG 1274
QY      381 AlaLysValGlyLeuTrpAspThrAspPheGlyLeuGlyLeuGlyLysProGluThrVal 400
Db      1275 GCCAAGTCGGACTCTGGGATTACGACTTTGGGTTCGGACTGGGTAAAGCCGAGACTGTG 1334
QY      401 ArgArgProIlePheGluProValGluSerLeuMetThrPheMetProLysLysProAsp 420
Db      1335 AGACGCCCAATCTTTGAGCGCTGTGAGAGCTGTGATCTTTATGCCCAAGAGCCTGAT 1394
QY      421 GlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAsp 440
Db      1395 GCGGAGTCTGTGCGGGCTTTCTCTGAGGATGAGGATGATGACCGATTGAAGGCGGAT 1454
QY      441 LysGluTrpThrLysThrAlaGlnTrpValGly 451
Db      1455 AAGGAGTGGACCAAGTATGCGCAGTACGTTGGT 1487

RESULT 4
AAAS4206
ID      AAAS4206 standard; cDNA; 1403 BP.
XX
AC      AAAS4206;
XX
DT      26-FEB-2001 (first entry)
XX
DE      Sequence encoding trichothecene resistance polypeptide.
XX
KW      Trichothecene resistance; resistant; crop protection; mycotoxin; fungus;
KW      wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;
KW      ds.
XX
OS      Fusarium sporotrichioides.
XX
FH      Key
FT      7.1386
FT      CDS
FT      /*tag= a
FT      /product= "Trichothecene resistance polypeptide"
XX
XX      WO200060061-A2.
XX
PD      12-OCT-2000.
XX
XX      29-MAR-2000; 2000WO-EP002769.
XX
XX      31-MAR-1999; 99US-00282995.
XX
XX      11-FEB-2000; 2000US-00502852.
XX
XX      (NOVS ) NOVARTIS AG.
XX
XX      (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX      Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;
XX
XX      WPI: 2000-679374/66.
XX
XX      P-PSDB; AAB03934.
XX
XX      Plant cell for preventing mycotoxin contamination of wheat, maize, barley
XX
XX      or rice plant, comprises heterologous polynucleotide encoding gene
XX
XX      product expressed in cell, having trichothecene resistance activity.
XX
XX      Claim 8; Page 46; 62pp; English..
XX
XX      A heterologous gene encoding a gene product which confers trichothecene
XX
XX      resistance can be used to transform plant cells to make them resistant to
XX
XX      fungal infection. The transformation method is useful for preventing
XX
XX      mycotoxin contamination of a plant, particularly a crop plant such as
XX
XX      wheat, maize, barley or rice, and for reducing and/or preventing the
XX
XX      growth of a fungus of the genus Fusarium that produces a trichothecene,

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CC      preferably comprising a C-3 hydroxyl group, by growing transformed crop
CC      plants in an area which is moderate to severe fungal infestation
XX
SQ      Sequence 1403 BP; 350 A; 397 C; 352 G; 304 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1,23e-172      Length:      1403
Score:          1860.50      Matches:      349
Percent Similarity: 88.67%      Conservative: 50
Best Local Similarity: 77.56%      Mismatches: 50
Query Match:    79.71%      Indels:      1
DB:            3      Gaps:      1

US-10-614-954-6 (1-451) x AAAS4206 (1-1403)

QY      2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTrpThr 21
Db      37 TCTTTTGACATAGAGCTCGACATCATCGCGCCAGCAACCCCTCTTCTTCAATCTACACC 96
QY      22 GlnIleSerLeuLeuTrpProValSerAspSerSerGlnTrpProThrIleValSerThr 41
Db      97 CAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCAGTATATCCCAACCATCGTCAGCACC 156
QY      42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61
Db      157 CTTGAGGAAGGCGCTAAACGCGCTCTCTCAACCTTCCCATGGGTCCGGCCAGGTCAG 216
QY      62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81
Db      217 ACCGAGGCGATCAGCGAGGAAACACAGGAACTTCCAGATCATTCATATGAGGAGACA 276
QY      82 ProArgValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet 101
Db      277 CCCCGTCTGTGGTGAAGACCTCGCTGATGATTCCTCAGCGCCACAGCATCGAGGGGTG 336
QY      102 ArgLysAlaGlyTrpProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr 121
Db      337 AGAAAGGCGGGTTCCTCCCTTAGAGATGTTTACGAGAACGTCGCTCCGAGGAAGACA 396
QY      122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141
Db      397 TTAGTATCGGACCTGGCAATGCGCCCAACGACCGAGCCGTGTGTCTATTGACAGTC 456
QY      142 AsnPheIleLysGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
Db      457 AACTTCATTAAAGGCGGACTCATTCACCGTCAACGCAACCATGGTGTATGGACATG 516
QY      162 ValGlyGlnAspAlaValIleArgLeuSerLysAlaCysArgAsnAspProPheThr 181
Db      517 ACAGGACAAAGATGCAATTATTCGTCTCTCAAGCGTCCGCAACCAATCATTCACC 576
QY      182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTrpLeuGluAsn 201
Db      577 GAGGAGGAATCTCGGCCATGAACTCGATCGCAGACGGTAGTCCCTCTCTTGAANAAC 636
QY      202 TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAsp 221
Db      637 TACAAAGTTGGTCTTGAGCTAGACCAACAGATCGCCAAACCTCGCGCTGCT---GGCGAC 693
QY      222 AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet 241
Db      694 GTCCACCCCGCCCGCCCAAGCAAGCTGGGGTCTTTTTCATTTCACTCCCAAGGCCCTC 753
QY      242 SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261
Db      754 TCGGAGCTGAAGAGCGCAGCCACCAAGACTTTGACCGCTGCTCCAAAGTTTGTGTCACT 813
QY      262 AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle 281
Db      814 GATGATGCTCTTTTCGGCGTTTATCTGGCAATCAACCTCGCGGTACGTCTCGCAAGATTG 873
QY      282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301

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Db 874 GATGCTTCCACACTACTGAATTCCTCCCGCGCTGTGCAACATGCGGGGCCCAATAGGGCGTA 933

Qy 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321
 |||:::|
 Db 934 TCAGACATACCAGCGCTTCTTCAAAACATGACCTACCATGACCTGCGACCGTCCGCGAA 993
 |||:::|
 Qy 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341
 |||:::|
 Db 994 ATGCGCAACGAACCACTTGGCGCAACAGCATCACGCTGCGCTCGGAACCTCAACAGTGAT 1053
 |||:::|
 Qy 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer 361
 |||:::|
 Db 1054 CGTTTGGCAGACGAAACACAGCTTTGGCGACGTATACATGCTGCGCTGTGCAAGTCG 1113
 |||:::|
 Qy 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381
 |||:::|
 Db 1114 AGCGTCTCCTGACCGCGGATGCGATCCGTCAAGCAGCATCATGTGAGTCTCTGGGCC 1173
 |||:::|
 Qy 382 LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg 401
 |||:::|
 Db 1174 AAGGTGGGATGCTGGGAGTATGACTTTGGGTTGGACTGGGTAAAGCCTGAGAGTGTGAGA 1233
 |||:::|
 Qy 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
 |||:::|
 Db 1234 AGACCTCGCTTTGAACCTTTTGAGAGTTTGATGTACTTTATGCCCAAGAGCCTGATGGG 1293
 |||:::|
 Qy 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441
 |||:::|
 Db 1294 GAGTTTACGGCGTCCATTTCTCGAGGGATGAGGATATGAGAGACTAAAGCGGATGAG 1353
 |||:::|
 Qy 442 GluTrpThrLysTyrAlaGlnTyrValGly 451
 |||:::|
 Db 1354 GAGTGACAAAGTACGCAAGTATATTGGG 1383
 |||:::|

RESULT 5
 ID AAA54213 standard; DNA; 12949 BP.

AC AAA54213;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE Transformation vector pNOV1704.
 XX
 KW Trichothecene resistance; resistant; crop protection; mycotoxin; fungus;
 KW wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;
 KW ds.
 XX
 OS Synthetic.
 XX
 XX WO200006061-A2.
 XX
 PD 12-OCT-2000.
 XX
 PF 29-MAR-2000; 2000WO-BP002769.
 XX
 XX 31-MAR-1999; 99US-00282995.
 PR
 PR 11-FEB-2000; 2000US-00502852.
 XX
 XX (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX
 XX Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;
 PI
 XX WPI; 2000-679374/66.
 DR
 XX Plant cell for preventing mycotoxin contamination of wheat, maize, barley
 PT or rice plant, comprises heterologous polynucleotide encoding gene
 PT product expressed in cell, having trichothecene resistance activity.
 XX
 PS Disclosure; Page 58-62; 62pp; English.
 XX
 XX A heterologous gene encoding a gene product which confers trichothecene

CC resistance can be used to transform plant cells to make them resistant to
 CC fungal infection. The transformation method is useful for preventing
 CC mycotoxin contamination of a plant, particularly a crop plant such as
 CC wheat, maize, barley or rice, and for reducing and/or preventing the
 CC growth of a fungus of the genus Fusarium that produces a trichothecene,
 CC preferably comprising a C-3 hydroxyl group, by growing transformed crop
 CC plants in an area which is moderate to severe fungal infestation. Plasmid
 CC pNOV1704 comprises the Zea mays ubiquitin promoter, the phosphate mannose
 CC isomerase selectable marker and the nopaline synthase termination
 CC sequence. pNOV1704 further comprises the Zea mays ubiquitin promoter
 CC operably linked to the trichothecene 3-O-acetyl transferase sequence
 CC given in GENESSEQ record AAA54206 and the nos termination sequence
 XX

SQ Sequence 12949 BP; 3194 A; 3146 C; 3143 G; 3466 T; 0 U; 0 Other;

Alignment Scores: 2,85e-171 Length: 12949
 Pred. No.: 1860.50 Matches: 349
 Score: 88.67% Conservative: 50
 Best Local Similarity: 77.56% Mismatches: 50
 Query Match: 79.71% Indels: 1
 DB: 3 Gaps: 1

US-10-614-954-6 (1-451) x AAA54213 (1-12949)

Qy 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21
 |||:::|
 Db 11282 TCTTTTGACATAGACTCGACATCATCGGCCAGCAACCGCTCTTCTTCACTACACC 11341
 |||:::|
 Qy 22 GlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThr 41
 |||:::|
 Db 11342 CAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCAGTATCCCAACCATCGTCAGCAC 11401
 |||:::|
 Qy 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61
 |||:::|
 Db 11402 CTTGAGGAGGCGCTAAACGCTCTCTCAACCTTCCCATGGGTGCGGGCCAGGTCAAG 11461
 |||:::|
 Qy 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81
 |||:::|
 Db 11462 ACCGAGGGCATCAGCGAGAGAAACACAGAACTTCCAGATCATTCATGAGGAGACA 11521
 |||:::|
 Qy 82 ProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet 101
 |||:::|
 Db 11522 CCCCCTCTGTGTGTAAGAACCTCGGTGATGATTCCTCAGCGCCCAACGATCGAGGGGTG 11581
 |||:::|
 Qy 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThr 121
 |||:::|
 Db 11582 AGAAGGCGGGTTTCCCTTTAGAGATGTTTGACGAGAAAGCTGCTCGTCCGAGGAGACA 11641
 |||:::|
 Qy 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141
 |||:::|
 Db 11642 TTAGCTATCGGACCTGGCAATGCGCCCAACGACCGAGCGCTGTGTGTTATTCAGCTC 11701
 |||:::|
 Qy 142 AsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
 |||:::|
 Db 11702 AACTTCATTAGGCGGAGCTCATTTCCCGTCAACGAGACACATGGTGTCTATGACATG 11761
 |||:::|
 Qy 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr 181
 |||:::|
 Db 11762 ACAGGACAAAGATGCAATTATTGCTTCTCTCAAGGCGTGGCCGCAACGATCATTCACC 11821
 |||:::|
 Qy 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsn 201
 |||:::|
 Db 11822 GAGGAGGAAATCTCGGCCATGAACCTCGATCGAAGACGGTAGTCCCTCTCTCTGAAAC 11881
 |||:::|
 Qy 202 TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAsp 221
 |||:::|
 Db 11882 TACAAAGTTGGTCTCTGAGCTAGACCACGATCGCAAACTCGCCCTGCT---GGCGAC 11938
 |||:::|
 Qy 222 AlaValLeuThrProValSerAlaSerTrpAlaPheThrPheSerProLysAlaMet 241
 |||:::|
 Db 11939 GCTCCACCGGACCCGCGCAAGCAAGCTGGGGTCTTTTTCATTCATCCCAAGGCCCTC 11998
 |||:::|

QY 242 SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261
 DB 11999 TCGAGCTGAAGACGACGACCAAGACTTTGACGCTCGTCCAAAGTTTGTGCACT 12058
 QY 262 AspAspAlaLeuSerAlaPheLeuTTPlysSerAlaSerArgValArgLeuGluArgIle 281
 DB 12059 GATGATGCTCTTTCGGCGTTTATCTGGCAATCAACCTCGCGGTACGTTCTGCAGATTG 12118
 QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaSerProAlaMetGlyVal 301
 DB 12119 GATGCTTCACACCTACTGAATTTCTCCGCGCTGTGCACATGCGGGGCCCAATGGCGTA 12178
 QY 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321
 DB 12179 TCAAGCACATACCCAGCGCTTCTTCAAAACATGACCTACCATGACTCGACCGCCGAA 12238
 QY 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341
 DB 12239 ATCGCCACGAACCACTTGGCGACAGCATCAAGCTCGCTCGGAACTCAACAGTGAT 12298
 QY 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer 361
 DB 12299 CGTTTGGCAGACGAACAGCTTTGGCGAGGTACATGATGCGCTGACCAAGTCG 12358
 QY 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381
 DB 12359 AGCGTCTCCCTGACCCCGATCGAATCGTCAAGCAGCATGATGCTGAGTTCTCTGGGCC 12418
 QY 382 LysValGlyLeuTTPAspTyrAspPheGlyLeuGlyLeuGlyLeuGlyProGluThrValArg 401
 DB 12419 AAGTGGGATGCTGGGAGTATGACTTTGGGTTGGACTGGTAAGCCTGAGAGTGTGAGA 12478
 QY 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
 DB 12479 AGACCTCGCTTTGAACCTTTTGAGAGTTTGATGTTACTTTATGCCCAAGAGCTGATGG 12538
 QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441
 DB 12539 GAGTTTACGGCGTCCATTTCTCTGAGGATGAGGATATGAGAGACTAAAGCGGATGAG 12598
 QY 442 GluTTPThrLysTyrAlaGlnTyrValGly 451
 DB 12599 GAGTGGCAAAAGTACGCAAGTATATTGGG 12628
 RESULT 6
 ID AAA54212 standard; DNA; 13737 BP.
 AC AAA54212;
 DT 26-FEB-2001 (first entry)
 DE Transformation vector pGROTRIR.
 XX Tricoothecene resistance; resistant; crop protection; mycotoxin; fungus;
 KW wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;
 KW ds.
 OS Synthetic.
 XX WO200006061-A2.
 PN 12-OCT-2000.
 PD 29-MAR-2000; 2000HO-EP002769.
 PF 31-MAR-1999; 99US-00282995.
 PR 11-FEB-2000; 2000US-00502852.
 XX (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;

XX WPI; 2000-679374/66.
 XX Plant cell for preventing mycotoxin contamination of wheat, maize, barley
 PT or rice plant, comprises heterologous polynucleotide encoding gene
 PT product expressed in cell, having tricoothecene resistance activity.
 XX Disclosure; Page 54-58; 62pp; English.
 XX A heterologous gene encoding a gene product which confers tricoothecene.
 CC resistance can be used to transform plant cells to make them resistant to
 CC fungal infection. The transformation method is useful for preventing
 CC mycotoxin contamination of a plant, particularly a crop plant such as
 CC wheat, maize, barley or rice, and for reducing and/or preventing the
 CC growth of a fungus of the genus Fusarium that produces a tricoothecene,
 CC preferably comprising a C-3 hydroxyl group, by growing transformed crop
 CC plants in an area which is moderate to severe fungal infestation. Plasmid
 CC pGROTRIR comprises a selectable marker operably linked to a promoter and
 CC terminator sequence and the tricoothecene resistance gene described in
 CC GENESSEQ record AAA54206 behind and in frame with the Arabidopsis thaliana
 CC UBI 3 promoter and in front of and in frame with the nos polyadenylation
 CC signal
 XX Sequence 13737 BP; 3341 A; 3442 C; 3629 G; 3325 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 3.1e-171 Length: 13737
 Score: 1860.50 Matches: 349
 Percent Similarity: 88.67% Conservative: 50
 Best Local Similarity: 77.56% Mismatches: 50
 Query Match: 79.71% Indels: 1
 DB: 3 Gaps: 1
 US-10-614-954-6 (1-451) x AAA54212 (1-13737)
 QY 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21
 DB 51 TCTTTTGACATAGACTCGACATCATCGGCCAGCAACCGCCTCTTCTTCAATCTACACC 110
 QY 22 GlnIleSerLeuLeuTyrProValSerSerSerGlnTyrProThrIleValSerThr 41
 DB 111 CAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCAGTATCCACCATCTGCAGACC 170
 QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTTPValAlaGlyGlnValLys 61
 DB 171 CTTGAGGAAGGCGCTAAACCGCTCTCTCAACCTTCCCATGGTTCGCGGCCAGGTCAAG 230
 QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81
 DB 231 ACCGAGGGCATCAGCAAGGAACACAGGAACCTTCCAGATCATTCATGAGGAGACA 290
 QY 82 ProArgValValValLysAspLeuArgAspProSerAlaProThrIleGluGlyMet 101
 DB 291 CCCGCTGTGTGTGTAAGACCTCGTGATGATTCCTCAGCCGCCAACGATCAGGGGTG 350
 QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThr 121
 DB 351 AGAAAGCGGGTTTCCCTTAGAGATGTTTACGAGAACGTCGCTCCGAGGAAGACA 410
 QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuGlnLeu 141
 DB 411 TTAGCTATCGGACCTGGCAATGGCCCAACGACCGGAGCCCTGTGTGTTATTCAGGCTC 470
 QY 142 AsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
 DB 471 AACCTTAAAGGGCGGACTCATTCACCGTCAACGGCAACATGGTCTATGACATG 530
 QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr 181
 DB 531 ACAGGACCAAGATGCAATATTCTCTCTCCTCAAGGGGTGCGGCAACGAATCATTCACC 590
 QY 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrThrGluAsn 201

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Db 591 GAGGAGAAATCTCGGCCATGAACCTCGATCGCAAGACGGTAGTCCCTCTCTTGTAAAAAC 650
QY 202 TyrThrIleGlyProGluValAspHisGlnIleValIysAlaAspValAlaGlyGlyAsp 221
Db 651 TACAAAGTTGGTCTGAGCTAGACCAACCAAGTCCCAAACTCGCGCTGCT---GGCGAC 707
QY 222 AlaValLeuThrProValSerAlaSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet 241
Db 708 GCTCCACCCGACCGGCAAGCAAGCTGGCGCTCTTTTCATTCATCCCAAGGCCCTC 767
QY 242 SerGluLeuIysAspAlaAlaThrLysThrLysLeuAspAlaSerThrLysPheValSerThr 261
Db 768 TCGAGCTGAAAGACGAGCAGCAAAAGACTCTTGACGCGCTCGTCCCAAGTTTGTCAACT 827
QY 262 AspAspAlaLeuSerAlaPheIleTyrLysSerAlaSerArgValArgLeuGluArgIle 281
Db 828 GATGATGCTCTTTCGGGGTTTATCTGGCAATCAACCTCGCGGTAGCTCTCGCAAGATTG 887
QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301
Db 888 GATGCTTCCACACCTACTGAATTCGCGCGCTGTCGACATGCGGGGCCCAATGGGCGTA 947
QY 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321
Db 948 TCAAGGACATATACCAGGCTTCTTCAAAACATGACCTACCATGCTCGACCGCTCGCGAA 1007
QY 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341
Db 1008 ATCGCCCAACGAACCATTTGGCGCAACAGATCAACGCTCGGCTCGGCAATCAACAGTAT 1067
QY 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer 361
Db 1068 CGTTTGGCAGACGAAACAAAGCTTTGGCGACGTACATGCTGCGCTGCAAGTCG 1127
QY 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381
Db 1128 AGGCTCTCCCTGACCCCGCATCGAATCCGTCAAGCAGCATCATGCTGATGTTCTCGGGCC 1187
QY 382 LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLysProGluThrValArg 401
Db 1188 NAGTGGGATCTGGGAGTATGACTTGGGTTGGACTGGGTAAAGCTGAGAGTGTGAGA 1247
QY 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
Db 1248 AGACCTCGCTTGAACCTTTGAGAGTTTCATGTACTTTATGCCCCAAGAAGCTGATGG 1307
QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441
Db 1308 GAGTTTACGGCGTCCATTCTCTGAGGATGAGGATATGGAGAGACTAAAGGCGGATGAG 1367
QY 442 GluTrpThrLysTyrAlaGlnTyrValGly 451
Db 1368 GAGTGACAAAGTACGCAAGTATATTGG 1397

RESULT 7
AAA54210
ID AAA54210 standard; DNA; 1425 BP.
XX
AC AAA54210;
XX
XX 26-FEB-2001 (first entry)
XX
DE Sequence encoding trichothecene resistance polypeptide.
XX
XX Trichothecene resistance; resistant; crop protection; mycotoxin; fungus;
KW wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;
KW ds.
XX
OS Saccharomyces cerevisiae.
XX
XX Key Location/Qualifiers
FH 1..1425
FT CDS /*tag= a
```

```
FT
XX
XX /product= "Trichothecene resistance polypeptide"
XX
XX WO2000060061-A2.
XX
XX 12-OCT-2000.
XX
XX 29-MAR-2000; 2000WO-EP002769.
XX
XX 31-MAR-1999; 99US-00282995.
XX
XX 11-FEB-2000; 2000US-00502852.
XX
XX (NOVS ) NOVARTIS AG.
XX
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;
XX
XX WPI; 2000-679374/66.
XX
XX P-PSDB; AAB03936.
XX
XX Plant cell for preventing mycotoxin contamination of wheat, maize, barley
XX or rice plant, comprises heterologous polynucleotide encoding gene
XX product expressed in cell, having trichothecene resistance activity.
XX
XX Claim 8; Page 50-51; 62pp; English.
XX
XX A heterologous gene encoding a gene product which confers trichothecene
XX resistance can be used to transform plant cells to make them resistant to
XX fungal infection. The transformation method is useful for preventing
XX mycotoxin contamination of a plant, particularly a crop plant such as
XX wheat, maize, barley or rice, and for reducing and/or preventing the
XX growth of a fungus of the genus Fusarium that produces a trichothecene,
XX preferably comprising a C-3 hydroxyl group, by growing transformed crop
XX plants in an area which is moderate to severe fungal infestation
XX
XX SQ Sequence 1425 BP; 431 A; 305 C; 293 G; 396 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,976-84 Length: 1425
Score: 962.50 Matches: 202
Percent Similarity: 62.86% Conservative: 84
Best Local Similarity: 44.40% Mismatches: 158
Query Match: 41.24% Indels: 11
DB: 3 Gaps: 8

US-10-614-954-6 (1-451) x AAA54210 (1-1425)
QY 6 GlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThrGlnIleSerLeu 25
Db 64 CAACTTGATATTTTGGGACAAACACCTTCGCTATACAACTATACACTCAATATGCTCT 123
QY 26 LeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThrPheGluGlnGly 45
Db 124 ATCTACCGTGACCAAGATCCTTCTGCTCATGACCATATCGTAATACTTAAACAGAGA 183
QY 46 LeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLysAlaGluGlyIle 65
Db 184 CTTGAACATTTGGCTAAAAATTTCCAGTGGGTAGCAGGAATGTCGTAATGAAGTGTCT 243
QY 66 SerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspValProArgValVal 85
Db 244 GACGAAGGTAACTGGGTACCTTACAGAAATTTGCCGTGAGCAAAATTTCCA---CTTATC 300
QY 86 ValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMetArgLysAlaGly 105
Db 301 GTCCAAGATCTTCGAGAAGATCTGTCTGCCCAACAATGGATTCTGCTTGAAAAAGCTGAC 360
QY 106 TyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThrLeu---ProIle 124
Db 361 TTTTCTATCTACATGTTAGACGAAAGAACTTTTGGCGCTTTCATGACTATCAATCCACT 420
QY 125 GlyProGlyThrGly---ProAspAspProLysProValIleLeuLeuGlnLeuAsnPhe 143
Db 421 GGAACACATATAGGTATGCGCGCCCAAGTGGGCTGTGATTTGCGGTTTCAAGCAACTTT 480
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Db 174 CTCTGCTTTCCGTTTCGATGCTCATCTGATCAC---GAGATAGTCAGGACCTAGAGAAT 230
Qy 45 GlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLysAlaGluGly 64
Db 231 GGCTCGAAGACTGTCCACAAATTCCTGGGTAGCAGCGCAGATAGTCAGTGAAGGC 290
Qy 65 IleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspValProArgVal 84
Db 291 AGCAGCCACAACTCTGGCACATTCATGATCAAGACCTGGGGAAGACTCCACCACTG 350
Qy 85 ValValLysAspLeuArgAspProSerAlaProThrIleGluGlyMetArgLysAla 104
Db 351 GTTGTGAAGACTTCCGTCATGATCCGACGTTCCGACCATGACGATTTGAGACGCGCC 410
Qy 105 GlyTyrProMetAlaMetPheAspGluAsnIleLeuAlaProArgLysThrLeuProIle 124
Db 411 GACTTTCCCTTCGGATGTTAGACGAGAACATCATGTCTCTCGGAAACCTTGCCA--- 467
Qy 125 GlyProGlyThrGlyProAspAspPro-----LysProValIleLeuLeuGlnLeuAsn 142
Db 468 -----AGCCCTGACGAGATATTTATCTCACCGGCTTTCTGTGTCAGGCTAAT 515
Qy 143 PheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMetVal 162
Db 516 TTTATTTACCGCGCGCTGTGCTCACTCTTTGTGGCCATCATAGCACAAATGGACATGACT 575
Qy 163 GlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThrGlu 182
Db 576 GGTGANGGACAGGTATTCACCTTCTCTCGAAGCATGTCTGGGGATACATATACAAGA 635
Qy 183 GluGluMetThrAlaMetAsnLeuAspArgLysThrIleValPro 197
Db 636 TTGGAGCTAGAGTCAGGAACTTAATGGAAGGTCACTCTGTTCCC 680

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RESULT 9

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ADE81194
ID ADE81194 standard; DNA; 1440 BP.
XX AC ADE81194;
XX 29-JAN-2004 (first entry)
DE Orf11 coding sequence, SEQ ID 22.
XX KW ML-236B; HMG-CoA reducing enzyme; ds; Orf11.
XX OS Penicillium citrinum.
XX Key Location/Qualifiers
FH 1. 1440
CDS /*tag= a
FT /product= "Orf11"
XX PN JP2003116567-A.
XX 22-APR-2003.
XX PF 15-OCT-2001; 2001JP-00316578.
XX PR 15-OCT-2001; 2001JP-00316578.
XX PA (SANY ) SANKYO CO LTD.
XX WPI; 2003-817677/77.
DR P-PSDB; ADE81195.
XX Novel DNA associated with synthesis of ML-236B, useful for improving ML-
PT 236B production in ML-236B producing microbe.
XX Example 8; SEQ ID NO 22; 142pp; Japanese.
XX The present invention relates to a DNA sequence (I, ADE81173), which is

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CC associated with ML-236B synthesis. (I) is useful for improving ML-236B
CC production in a HMG-CoA reducing-enzyme-inhibitor ML-236B producing
CC microbe. The present sequence was used to illustrate the invention.
XX
SQ Sequence 1440 BP; 336 A; 359 C; 367 G; 378 T; 0 U; 0 Other;

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Alignment Scores:

```

Pred. No.: 6,55e-25 Length: 1440
Score: 356.50 Matches: 129
Percent Similarity: 44.44% Conservatives: 87
Best Local Similarity: 26.54% Mismatches: 183
Query Match: 15.27% Indels: 87
DB: 10 Gaps: 20

US-10-614-954-6 (1-451) x ADE81194 (1-1440)
Qy 25 LeuLeuTyrProValSerAspSerGlnTyrProThrIleValSerThrPheGluGln 44
Db 58 CTGTGTTCCCTCACTCGGATGCATCA---ATTCCGCAAACTGTTTCAGTCTCTCGGGAG 114
Qy 45 GlyLeuLysArgPheSerGluAlaValProTyrValAlaGly-----GlnValLys 61
Db 115 GGACTCTCCAGGTTTATCCCAAGTTTACTATTCTTCTAGTGGCAACCTCAGCAAGTCGAA 174
Qy 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleVal-----ProPhe 78
Db 175 AATGCTGGGCTCAGACCTGGA-----AGTTTCGCGTGAATCAAAACCATCC 222
Qy 79 GluAspValProArgValValValLysAspLeuArgAspAspProSerAlaPro----- 96
Db 223 GAGCCG---CCTACCTCTTTCAGTTCGAGACATGACGAGCGGCTCTAGTACAGATTGGAGT 279
Qy 97 ---ThrIleGluGlyMetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIle 115
Db 280 TGGACATACCATGATCTCCGTGAACGGGATTTCCATGAGTCTGCTGACCGGACGTT 339
Qy 116 IleAlaProArgLysThrLeuProIleGlyThrGlyProGlyProAspAspProLysPro 135
Db 340 CTCGCCCG-----ACTGATCCCTGTTTCAGGGGTACA 372
Qy 136 ValIleLeu---LeuGlnLeuAsnPheIleLysGlyLeuIleIleuThrValAsnGly 154
Db 373 AGACTCTTGGCTGCAAGCAAAATTCATTCGGGAGGCTGCCTGTTATACCTCTCAACC 432
Qy 155 GlnHisGlyAlaMetAspMetValGlyGlnAspAlaValIleArgLeuLeuSerLysAla 174
Db 433 TCGCAGCGCTTCGCGGACGCTTGGACTCTCTACCTTGTCTATGTGAGTGGAGTCGGCAA 492
Qy 175 CysArgAsnAspProPheThrGluGluMet----- 185
Db 493 TGCCGTGATGCTCTTGGCACCAGTACGAAATACCGAATGTTAGCAGGCGAGAAGAAATT 552
Qy 186 ---ThrAlaMetAsnLeuAsp-----ArgLysThrIleVal---ProTyrLeuGlu 200
Db 553 TCCACGGCATTTGGATCAAGACTCGCCCTGTGTCAGCTAGTGTGTTCAACCTTATAGTCCC 612
Qy 201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly 220
Db 613 AGCTCAGCGGTCTATGAGCGTCTCAAAATCCAAACCAATTCGTGGCATGTTTGGGGTTG 672
Qy 221 Asp-----AlaValLeuThrProValSer 228
Db 673 GATTGGAGACCCAAAGAACGACGATGCGGATTTGATGTCTCAGATCCCTCCGCGCT 732
Qy 229 AlaSerTrpAlaPhePheThrPheSerProLysAlaMetSerGluLeuLysAspAla 248
Db 733 GTGAGGTGCTATATTCTTATTTACCCAAATTCGTGAGAAAGTTGAGGCAAGTGGCT 792
Qy 249 -----ThrLysThrLeuAspAlaSerThrLysPheValSerThrAspAlaLeu 265
Db 793 CTAGGGGGGTCTTCTGGTGTCTCCAAATCTTCACAGTCTATTTCACGCGAGCATGCACTG 852
Qy 266 SerAlaPheIleTrpLysSerAlaSerArgValArgLeu---GluArgIleAspGlySer 284

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Db 853 GGGCCCTGCTTTGGAGCTGCTTATGAGAGCTCGTTTACGGAACGAGAAAGTTTCGAG 912
Qy 285 AlaProThrGlu-----PheCysArgAlaValAlaArgProAlaMetGlyValSer 302
Db 913 AACCCCAAGAGACGACATGATGCGCGGTCAACGTGGCAACTCTGTCTGTCCA 972
Qy 303 AsnAsnTyrProGly-----Leu 308
Db 973 GAAACACATCTTGGCAACACGATTTTATGCGGTGACAAAGCTGTCATTGATCTGCTC 1032
Qy 309 LeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGluIleAlaAsnGluSerLeuGly 328
Db 1033 GCCACTAGGGGCACAGACCATTTGAATGTTGTCTCAGAGTTTGGCGGAATCTCTC--- 1089
Qy 329 AlaThrAlaSerArgLeuArgSerGluLeuAspProAlaSerMetArgGlnArgThrArg 348
Db 1090 -----GACGAGCTGAGAGACTCTAGTATGTTTCAAGAGCGGTA 1128
Qy 349 GlyLeuAlaThrTyrLeuHisAsnProAspLysSerAsnValSerLeuThrAlaAsp 368
Db 1129 GAATTTGGCA-----AACACATCCCGGATGTCGGCGCATGGGACTCTCATTTCC 1179
Qy 369 AlaAspProSerThrSerValMetLeuSerSerTyrAlaLysValGlyLeuTyrAspTyr 388
Db 1180 ACCTGGGTTGCGGAGAACATGGTGTAGTTCTTCTCGATTGCGCTACTAGACTGG 1239
Qy 389 AspPheGlyLeu-----GlyLeuGlyLysProGluThrValArgArgProIle 404
Db 1240 GATTTCGGAAGTATATCTACGGGGGCTTGGGACCGGACAGATGGATGCCCTCCC--- 1296
Qy 405 PheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGlyGluPheCys 424
Db 1297 GACAACTGTTTGAAGGTATAACCTTTACTATGCCCGCAGCGACGACGATCACTGGAA 1356
Qy 425 AlaAlaLeuSerLeuArgGluAspMetAspArgLeuLysAlaAspLysGluTyrThr 444
Db 1357 ATCATGATCACCATGAAGACGATGGATATGGAGATATTGATACCGATCAAACTTCACT 1416
Qy 445 LysTyrAlaGlnTyrVal 450
Db 1417 GAGTTCTTCAGCTTTGTA 1434

RESULT 10
ID ADE81173
XX ADE81173 standard; DNA; 72149 BP.
AC ADE81173;
DT 29-JAN-2004 (first entry)
XX ML-236B synthesis related DNA sequence, SEQ ID 1.
DE ML-236B; HMG-CoA reducing enzyme; ds.
KW ML-236B; HMG-CoA reducing enzyme; ds.
XX Penicillium citrinum.
OS JP2003116567-A.
XX 22-APR-2003.
PD 15-OCT-2001; 2001JP-00316578.
XX 15-OCT-2001; 2001JP-00316578.
PR (SANY ) SANKYO CO LTD.
PA WPI; 2003-817677/77.
XX Novel DNA associated with synthesis of ML-236B, useful for improving ML-
XX 236B production in ML-236B producing microbe.
PT Claim 1; SEQ ID NO 1; 142pp; Japanese.
PS

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XX The present invention relates to a DNA sequence (I, ADE81173), which is
CC associated with ML-236B synthesis. (I) is useful for improving ML-236B
CC production in a HMG-CoA reducing-enzyme-inhibitor ML-236B producing
CC microbe.
XX Sequence 72149 BP; 18531 A; 17735 C; 17402 G; 18481 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.65e-22 Length: 72149
Score: 356.50 Matches: 129
Percent Similarity: 44.44% Conservative: 87
Best Local Similarity: 26.54% Mismatches: 183
Query Match: 15.27% Indels: 87
DB: 10 Gaps: 20
US-10-614-954-6 (1-451) x ADE81173 (1-72149)
Qy 25 LeuLeuTyrProValSerAspSerGlnTyrProThrIleValSerThrPheGluGln 44
Db 24167 CTGTGTTTCCCTCACTCGGATGCATCA---ATTCCGCAAACTGTTTTCAGTCTCTCGGGAG 24223
Qy 45 GlyLeuLysArgPheSerGluAlaValProTyrValAlaGly-----GlnValLys 61
Db 24224 GGACTCTCAAGCTTTATGCCAAGTTACTATTCTTACTGGCAACCTCCAGCAAGTCGAA 24283
Qy 62 AlaGluGlyIleSerGluAsnThrGlyThrSerPheIleVal-----ProPhe 78
Db 24284 AATGCTGGGCTCAGACCTGGA-----AGTTTCGCGTGGAAATCAAAACCATCC 24331
Qy 79 GluAspValProArgValValLysAspLeuArgAspProSerAlaPro-----96
Db 24332 GAGCCG---CCTACCTTTTCAGTTCGAGACATGACGAGCGGCTCTAGTACAGATTGGAGT 24388
Qy 97 ---ThrIleGluGlyMetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIle 115
Db 24389 TGGACATACCATGATCTCCGTGAACGGGATTTCCATGAGTCTGCTAACCGGAGCTT 24448
Qy 116 IleAlaProArgLysThrLeuProIleGlyProGlyThrGlyProAspProLysPro 135
Db 24449 CTCGCCCG-----ACTGATCCCTGTTTCAGGCGGTACA 24481
Qy 136 ValIleLeu---LeuGlnLeuAsnPheIleLysGlyLeuIleLeuThrValAsnGly 154
Db 24482 AGACTCTTGGCTGCACAAAGAAATTTTCATTCGGGAGGCTGCTGTATATACGTTCAACC 24541
Qy 155 GlnHisGlyAlaMetAspMetValGlyGlnAspAlaValIleArgLeuSerLysAla 174
Db 24542 TCGCAGCGCTTCGGGACGCGCTTTGGACTCTCTACCTTCTGTATGTGAGTGGAGTCGGCAA 24601
Qy 175 CysArgAsnAspProPheThrGluGluMet-----185
Db 24602 TCCCGTGTGCTCTTGGCACCATGACGAAATACCGAATGTTAGCAGGAGGAGAAAT 24661
Qy 186 ---ThrAlaMetAsnLeuAsp-----ArgLysThrIleVal---ProTyrLeuGlu 200
Db 24662 TCCACGGCATTTGGATCAAGACTCGCCTGTCGAGCTAGTCTGTTTCAACCTATAGTCCC 24721
Qy 201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGly 220
Db 24722 AGTCAGCGGTCTATGAGCGTCTCAAAATCAAAACCAATTTCTGTGGCATGTTTGGGGTTG 24781
Qy 221 Asp-----AlaValLeuThrProValSer 228
Db 24782 GATTGGAGACCCAAAGAACGACGAGCTCGGATATTGATGCTCTCAGATCCCTCGTGCCT 24841
Qy 229 AlaSerTrpAlaPhePheThrPheSerProLysAlaMetSerGluLeuLysAspAlaAla 248
Db 24842 GTGAGTCTGTGTATATTCTCTATTACCGCAAAATTTCTGTGAGAAAGTTGAGCAAGTGGCT 24901
Qy 249 -----ThrLysThrLeuAspAlaSerThrLysPheValSerThrAspAlaLeu 265
Db 24902 CTAGGGGGGTCTTCTGGTGTTCAAAATCTTCCAGTCTTATTTCACGACGATGCACTG 24961

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QY 266 SerAlaPheIleTriPlysSerAlaSerArgValArgLeu---GluArgIleAspGlySer 284
DB 24962 GGGCCCTGCTTGGAGCTGCCTTATGAGAGCTCGTTGACGGAAGAGAAAGTTTCGAG 25021
QY 285 AlaProThrGlu-----PheCysArgAlaValAspAlaArgProAlaMetGlyValSer 302
DB 25022 AACCCCAAGGACGACAAATGATGCGAGCGGTCAACGTGCGCAAACTCCTGCTGTTC 25081
QY 303 AsnAsnTyrProGly-----Leu 308
DB 25082 GAAACACATCTTGGCAACACGATCTTTATGCGGTGACAAAGCTGTCATTGATCGCTC 25141
QY 309 LeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGluIleAlaAsnGluSerLeuGly 328
DB 25142 GCCACTAGGGGCACACACATTGATGTGTGCTCAGAGTTGGCGGAATCTCTC--- 25198
QY 329 AlaThrAlaSerArgLeuArgSerGluLeuArgSerProAlaSerMetArgGlnArgThrArg 348
DB 25199 -----GACGAGCTGAGAGACTCTAGTATGTTGTTCAAGAGCGGTA 25237
QY 349 GlyLeuAlaThrTyrLeuHisAsnProAspLysSerAsnValSerLeuThrAlaAsp 368
DB 25238 GAATTGGCA-----AACAACTCCCGGATGTCGCGGATGGGACTCTCATTTTCCC 25288
QY 369 AlaAspProSerThrSerValMetLeuSerSerTrpAlaLysValGlyLeuTrpAspTyr 388
DB 25289 ACGTGGTTCGGGAGAACATGTGTAGTTCTCTTCGATGCGCTACTAGACTGG 25348
QY 389 AspPheGlyLeu-----GlyLeuGlyLysProGluThrValArgArgProIle 404
DB 25349 GATTCGGAAGTATATCTCACGGGGCTTGGGCAAGCGGACAGAAATGCGATTCGCC--- 25405
QY 405 PheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGlyGluPheCys 424
DB 25406 GACAAAGTGTGTTGAAGGTATAACCTTTACTATGCCCGCCAGCGACCGATCATG 25465
QY 425 AlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLysGluTrpThr 444
DB 25466 ATCATGATCACCATGAAGACAGTGGATATGGAGATATTGATGACCGATCAACCTTCACT 25525
QY 445 LysTyrAlaGlnTyrVal 450
DB 25526 GAGTTCCTCAGCTTTGTA 25543
RESULT 11
ABZ54817
ID ABZ54817 standard; cDNA; 482 BP.
XX
AC ABZ54817;
XX
DT 28-MAR-2003 (first entry)
XX
DE Aspergillus oryzae polynucleotide SEQ ID NO 3930.
XX
KW Aspergillus oryzae; fermentation; fungus; industrial; EST;
XX expressed sequence tag; gene; ss.
XX
OS Aspergillus oryzae.
XX
PN WO200279476-A1.
XX
PD 10-OCT-2002.
XX
PF 22-MAR-2002; 2002WO-IB000890.
XX
PR 30-MAR-2001; 2001JP-00098371.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX (NARE-) NAT RES INST BREWING.
XX (NOR) NAT FOOD RES INST MIN AGRIC.
XX
PI Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;
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PI Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;
XX WPI; 2003-046817/04.
XX
PT Detection of expression of specific aspergillus genes for monitoring the
XX fermentation and growth conditions of the fungus, using DNA probes.
PS Claim 1; SEQ ID NO 3930; 48pp + Sequence Listing; Japanese.
XX
CC The invention relates to a polynucleotide having any of 6006 specific
CC sequences (ABZ50888-ABZ56893), which are expressed by a fungus under
CC specific culture conditions including one or more of eutrophic,
CC oligotrophic, solid, early germination, alkaline, high temperature, low
CC temperature or maltose culture or polynucleotides stringently hybridising
CC to these sequences. The polynucleotides are useful for monitoring the
CC progress of fermentation and the growth conditions of a fungus,
CC especially of Aspergillus oryzae which is widely used in industrial
CC fermentation. Also monitoring for fungal contamination. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 482 BP; 131 A; 109 C; 115 G; 127 T; 0 U; 0 Other;
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Alignment Scores:

Pred. No.:	4.84e-25	Length:	482
Score:	351.00	Matches:	66
Percent Similarity:	74.50%	Conservative:	22
Best Local Similarity:	55.93%	Mismatches:	28
Query Match:	8	Indels:	2
DB:		Gaps:	1

US-10-614-954-6 (1-451) x ABZ54817 (1-482)

QY 335 ArgSerGluLeuAspPro-----AlaSerMetArgGlnArgThrArgGlyLeuAlaThr 352

DB 3 AGAATGGCAATAGACCCGACAGCTCTTCTTTAAGTCTCGCACCCGCGCTAGCGACA 62

QY 353 TyrLeuHisAsnAsnProAspLysSerAsnValSerLeuThrAlaAspAlaAspProSer 372

DB 63 TACATTGAGTCTCTCGTAGACAAATCGTCCATCTCTTCGGAGCGAGTTTCAATCCCTCG 122

QY 373 ThrSerValMetLeuSerSerTrpAlaLysValGlyLeuTrpAspTyrAspPheGlyLeu 392

DB 123 ACGGATATTATTATGATGCTCGTGGCAAGTGTCAATGCTATCAATTAGACTTCGGATTTC 182

QY 393 GlyLeuGlyLysProGluThrValArgArgProIlePheGluProValGluSerLeuMet 412

DB 183 GGCCCTTGGAAAGCCGGAGGCTGTGCGACGACCGCAATTCCTCCGTTGAAGGTTGATT 242

QY 413 TyrPheMetProLysLysProAspGlyGluPheCysAlaAlaLeuSerLeuArgAspGlu 432

DB 243 TATTTTCATGCCCAAGAGGTCTGATGGCGAGATTGCTGTGCTCTCGTTACAGGAGGAG 302

QY 433 AspMetAspArgLeuLysAlaAspLysGluTrpThrLysTyrAlaGlnTyrVal 450

DB 303 GATATGGCGCGGTTGGCGCGGATGAAGAGTTTACGAGTTTGGCAAAATATATC 356

RESULT 12

ADO70366

ID ADO70366 standard; cDNA; 1508 BP.

XX

AC ADO70366;

XX

DT 12-AUG-2004 (first entry)

XX

DE Barley agmatine coumaroyltransferase coding sequence.

XX

KW barley; ss; gene; agmatine coumaroyltransferase; ACT; antimicrobial;

XX pathogen resistance; enzyme.

XX

OS Hordeum vulgare.

XX

ABX78350
ID ABX78350 standard; cDNA; 1587 BP.

XX AC ABX78350;

XX DT 14-APR-2003 (first entry)

XX XX Wheat stress response protein EST #6.

XX KW Plant; ss; EST; expressed sequence tag; stress response; drought; heat;
XX KW radiation; pathogen attack; grain flavour; disease resistance;
XX KW peptide-methionine sulfoxide reductase; DNA repair;
XX KW intracellular protein transport.

XX OS Triticum aestivum.

XX PN US2002152497-A1.

XX PD 17-OCT-2002.

XX PF 19-FEB-2002; 2002US-00078929.

XX PR 07-MAY-1999; 99US-0133038P.

XX PR 07-MAY-1999; 99US-0133042P.

XX PR 11-MAY-1999; 99US-0133427P.

XX PR 11-MAY-1999; 99US-0133428P.

XX PR 11-MAY-1999; 99US-0133436P.

XX PR 11-MAY-1999; 99US-0133437P.

XX PR 11-MAY-1999; 99US-0133438P.

XX PR 04-JUN-1999; 99US-0137667P.

XX PR 05-MAY-2000; 2000US-00566394.

XX (FALC/) FALCO S C.

PA (FAMO/) FAMODU O O.

PA (WEYE/) MEYERS B C.

PA (MIAO/) MIAO G.

PA (ODEL/) ODELL J T.

PA (RAFA/) RAFALSKI J A.

PA (THOR/) THORPE C J.

PA (SAKA/) SAKAI H.

PA (WENG/) WENG Z.

XX PI Falco SC, Famodu OO, Meyers BC, Miao G, Odell JT, Rafalski JA;

PI Thorpe CJ, Sakai H, Weng Z;

XX DR WPI; 2003-198391/19.

XX DR P-PSDB; ABU58179.

XX DR New peptide-methionine sulfoxide reductase and nucleic acids, useful in
PT improving plant response to stress, engineering plants with increased
PT disease and stress resistance, or and improving/protecting grain-flavor.

XX PS Disclosure; Page 71-72; 205pp; English.

XX CC The invention relates to isolated nucleic acids encoding plant stress
CC response proteins (including peptide-methionine sulfoxide reductases)
CC appearing as ABU58148-ABU58246 (or a protein 80% identical to them) from
CC Zea mays, Oryza sativa, Glycine max, or Triticum aestivum. Also included
CC are expression cassettes, transformed host cells, transgenic
CC plants/seeds, modulating the level of peptide-methionine sulfoxide
CC reductase in a plant and a computer system/data processing system for
CC identifying, analysing, or modelling a genetic sequence. The plant
CC nucleic acid is useful in developing strategies to improve plant response
CC to stress (e.g. drought, heat, radiation or pathogen attack), engineering
CC plants with increased disease and stress resistance, manipulating DNA
CC repair and recombination efficiency, manipulating intracellular protein
CC transport, and improving/protecting grain flavour. The nucleic acids may
CC also be used as probes or amplification primers in the detection,
CC quantitation or isolation of gene transcripts, for recombinant expression
CC of encoded polypeptides, as immunogens in preparing or screening
CC antibodies, and in sense or antisense suppression of one or more genes in
CC a host cell, tissue or plant. The proteins may be used as immunogens or
CC antigens to obtain antibodies specifically immunoreactive with the

CC protein, and in assays for enzyme agonists or antagonists. The present
CC sequence is a plant stress response cDNA or fragment (EST, expressed
CC sequence tag)

XX SQ Sequence 1587 BP; 287 A; 499 C; 525 G; 276 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.39e-06 Length: 1587
Score: 170.50 Matches: 84
Percent Similarity: 35.19% Conservatives: 61
Best Local Similarity: 20.39% Mismatches: 158
Query Match: 7.31% Indels: 109
DB: 10 Gaps: 15

US-10-614-954-6 (1-451) x ABX78350 (1-1587)

QY 56 ValAlaGlyGlnValLysAlaGluGlyIleSerGluGlyAsn----- 59

DB 275 CTGGCGGGCGCTCTGGCGGAGAGGCG-----GAGGGCGGGGTGCAGATCGACTGC 328

QY 70 ThrGlyThrSerPheIleValProPheGluAspValProArgValValLysAspLeu 89

DB 329 AACGGGAGGAGCGCTCTCTCTCCGCCAGGGCGCGAGCTCCCGGGGAGACCTC 388

QY 90 ArgAspAspProSerAlaProThrIleGluGlyMetArgLysAlaGlyTyrProMetAla 109

DB 389 TTCGGGAGCGGTACGAGCCCTCGCGGAG---ATCAGGCGGATGTCGTGCCCTTCGCG 445

QY 110 MetPheAspGluAsnIleAlaProArgLysThrLeuProIleGlyProGlyThrGly 129

DB 446 -----CCCTCCGCG----- 454

QY 130 ProAspAspProLysProValIleLeuLeuGlnLeuAsnPheIleLys---GlyGlyLeu 148

DB 455 ---GACCCGCCCTGCATATGCGCATGTTCAGGTGAGCTTCTCAAGTCGGCGGGCGG 511

QY 149 IleLeuThrValAsnGlyGlnHisGlyAlaMetAspMetValGlyGlnAspAlaValIle 168

DB 512 GTGCTGGGCACGGGATCCACCACGTGACCATGAGCGGCGGCGGTCCTCCTTCATC 571

QY 169 ArgLeu-----LeuSerLysAlaCysArgAsnAspPro 179

DB 572 CAGACATGACGGGTCTCGCGGGGGGTCTCCCTCTCCGAGCGGTGCGCGCGCGCG 631

QY 180 PheThrGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeu 199

DB 632 TTCCACGACCGCAGCTCTCTCGCGCGGCGCGCGCGCG----- 673

QY 200 GluAsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGly 219

DB 674 -----CCGGAATTCGAGCACCCTGCTACTCGCGCGCGGTACCTCAAC 715

QY 220 GlyAspAlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLys 239

DB 716 GGC-----GCCCCACGGCCCTTCTGTCACCCCGGTCTACTCTGTTCCAGAG 763

QY 240 AlaMetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheVal 259

DB 764 CTCCTCGCGGACATCAAGTCCCGGGCGCGCGCTGC-----GTG 802

QY 260 SerThrAspAspAlaLeuSerAlaPheIleThrLys----- 271

DB 803 TCCACTACGGCGCGGTGACCGCGCACCTCTGGCGCTGCATGTGCGCGCGCGGGCTC 862

QY 272 -----SerAlaSerArgValArgLeu-----GluArgIleAspGly 283

DB 863 GTCGCGGCTCGACACCGGCTCTCGGTGGCGGCAACATCCCGCACCGCTGCGCGCG 922

QY 284 SerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyValSerAsn 303

DB 923 CAGCTCCCGCGCGAGTCTCTCGGCAACCCATCGTGGCGCGCGTCCGTCAACG--- 979

QY 304 AsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGluIleAla 323

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Alignment Scores:		
Pred. No.: 1.4e-06 Length: 1596		
Score: 170.50 Matches: 107		
Percent Similarity: 36.68% Conservative: 61		
Best local Similarity: 23.36% Mismatches: 153		
Query Match: 7.31% Indels: 137		
DB: 3 Gaps: 25		
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DB	182	CCACCGCGCTTCCCAATTTCTTTCACCTCAGGTCATGAGGAGAGCTCTTTCCAAAGCC 241
QY	53	---ValProTrp-----ValAlaGlyGlnValLysAlaGluGly----- 64
DB	242	CTTGTCCTTTTACCTATGCTGCTGCTGAGAGAGACGATGCTGCTATTGAG 301
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DB	302	ATCGATTGTACGGTCCGGTCTCTTCGTTGTT-----GCTGATACTCCTTCTGTT 355
QY	85	ValValLysAspLeuArgAspAsp-----ProSerAlaProThrIleGluGlyMetArg 102
DB	356	ATC-----GATGATTTGTGTGATTGTGCTCTACCCTT----- 388
QY	103	LysAlaGlyTyPzProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThrLeu 122
DB	389	-----AATCTC-----CGTCAGCTTATT 406
QY	123	Pro---IleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141
DB	407	CCCGAAGTTGATCACTCCACCGCATTCACCTCT---TTCCCGCTTCTCGTTTTCAGAGTG 463
QY	142	AsnPheIleLys---GlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAsp 160
DB	464	ACTTTCTTTAAATGGGGGAGCTTCACCTTGGGTTGGGATCGACATCACCGGCAGAT 523
QY	161	MetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPhe 180
DB	524	GGTTTCTCTGGTCTTCATTTTATCAACACATGCTGATGCTCGT----- 571
QY	181	ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGlu 200
DB	572	-----GGTCTTGAC----- 580
QY	201	AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAla----- 215
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QY	216	-----AspValAlaGlyGlyAsp 221
DB	638	CCTGCTTTTTCATGTTGAATATCAGCTCGCCACCAAGTATGAAGATCCCTCTTGATCCA 697
QY	222	AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet 241
DB	698	TCCAAATCAGGACCTCAGAATACCACCGTGTCTATATTCAAATTAACAGACACCGAGCTT 757
QY	242	SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261
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QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAla-----ArgPro 297
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QY 298 AlaMetGlyValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSer 317
DB 926 CAGCTCGCT-----CCTGGTTACTTTGGGAATGTGATATTCACTGCAACA 970
QY 318 ThrIle-----GlyGluIle 322
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QY 323 AlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAlaSer 342
DB 1031 CATGATTTCTTGGTTCGTATGGATGATACTATCTGAGGTCAGCTCTTGAC----- 1081
QY 343 MetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSerAsn 362
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QY 363 ValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAlaLys 382
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QY 383 ValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArgArg 402
DB 1172 TTACCTATTATGATGCAGACTTGGTTGGGT-----CGT 1207
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XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 61174.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
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OS Arabidopsis thaliana.
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PN EP1033405-A2.
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QY 243 GluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThrAsp 262
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QY 263 AspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIleAsp 282
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QY 299 MetGlyValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThr 318
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Search completed: January 24, 2005, 06:13:40
Job time : 748 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 24, 2005, 01:46:06 ; Search time 4360 Seconds

(without alignments)
3769.339 Million cell updates/sec

Title: US-10-614-954-6

Perfect score: 2334

Sequence: 1 MAFKIQDLPGLGGLLSIY.....EDMDRLKADKWKYAYVG 451

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
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-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG
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Database :

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2: gb_est2: *
3: gb_hcc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_g881: *
9: gb_g882: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	694	29.7	508	BI191865	BI191865 l3b10fs.r
4	672	28.8	498	BI200717	BI200717 ole06fs.r
5	648	27.8	1055	BI947129	BI947129 HVSMEL1000
6	644	27.6	499	BI191678	BI191678 l1fl1fs.f
7	601	25.7	481	BI191864	BI191864 l3b10fs.f
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C	13	530.5	22.7	392	4	BI192452	BI192452 m4b09fs.r
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C	15	526	22.5	423	4	BI192498	BI192498 m4f10fs.f
C	16	506.5	21.7	374	4	BI187896	BI187896 b3c09fs.f
C	17	490	21.0	401	4	BI188598	BI188598 d1fl1fs.f
C	18	490	21.0	401	4	BI192451	BI192451 m4b09fs.f
C	19	490	21.0	490	4	BI201353	BI201353 p2e13fs.r
C	20	484	20.7	393	4	BI188605	BI188605 d1g04fs.f
C	21	478	20.5	372	4	BI192380	BI192380 m3e10fs.f
C	22	469	20.1	348	4	BI191129	BI191129 j3e01fs.r
C	23	468	20.1	476	4	BI192381	BI192381 m3e10fs.f
C	24	459	19.7	358	4	BI201146	BI201146 o4h01fs.f
C	25	456.5	19.6	336	4	BI191040	BI191040 j2h03fs.r
C	26	451	19.3	350	4	BI190499	BI190499 l2a07fs.f
C	27	447	19.2	459	4	BI187539	BI187539 a4e05fs.r
C	28	429	18.4	330	4	BI191128	BI191128 j3e01fs.f
C	29	413	17.7	435	4	BI187304	BI187304 a2b09fs.r
C	30	405	17.4	318	4	BI192335	BI192335 m3b01fs.f
C	31	392	16.8	303	4	BI189964	BI189964 g3b07fs.f
C	32	392	16.8	304	4	BI190847	BI190847 j1d11fs.f
C	33	392	16.8	308	4	BI188363	BI188363 c4a03fs.f
C	34	392	16.8	308	4	BI190145	BI190145 g4e10fs.f
C	35	385	16.5	311	4	BI200611	BI200611 n4e05fs.f
C	36	383	16.4	303	4	BI188705	BI188705 d2e07fs.f
C	37	370	15.9	385	4	BI189867	BI189867 g2d04fs.r
C	38	340	14.6	270	4	BI188630	BI188630 d1h09fs.f
C	39	338	14.5	841	9	CNS060HK	AL410670 T7 end of
C	40	336	14.4	278	4	BI191799	BI191799 l4f11fs.f
C	41	323	13.8	260	4	BI191495	BI191495 k4b11fs.f
C	42	323	13.8	352	4	BI188631	BI188631 d1h09fs.r
C	43	323	13.8	352	4	BI201565	BI201565 g2c06fs.r
C	44	323	13.8	360	4	BI187939	BI187939 b3f01fs.r
C	45	323	13.8	361	4	BI201147	BI201147 o4h01fs.r

ALIGNMENTS

BI949616 899 bp mRNA linear EST 19-OCT-2001
HVSMEL10014017f Hordeum vulgare spike EST library HVCDNA0012
(Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone
HVSMEL10014017f, mRNA sequence.

BI949616 GI:16291032

ACCESSION

VERSION

SOURCE

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Wing RA

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Total hg bases = 598

Seq primer: AATTAACCTCTACTAAGGG

High quality sequence stop: 755.

Location/Qualifiers

FEATURES

```

source
1. .899
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Morex"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HVSME10014017f"
/tissue_type="Spike"
/lab_host="TJC121"
/clone_lib="Hordeum vulgare spike EST library HVCDNA0012
(Fusarium infected)"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Plants were grown at the University of Minnesota in
the GJ Muehlbauer lab; spikes were harvested and snap
frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium
graminearum inoculation (Heinen). In the TJ close lab at
the University of California, Riverside, total RNA was
prepared from each sample pool, equal quantities of all
eight RNA pools were combined, poly(A) RNA was purified
from the mixture, one primary unamplified cDNA library was
made, and 1 million pfu were in vivo excised to give
pBluescript SK(-) cDNA phagemids (Choi, Fenton,
Malatrasi). Phagemids were plated and picked at the
Clemson University Genomics Institute (CUGI) (Begum,
Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,
Oates, Rambo, Main). The sequence has been trimmed to
remove vector sequence and contains a minimum of 100 bases
of phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:23-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

ORIGIN
Alignment Scores:
Pred. No.: 3,56e-113 Length: 899
Score: 1132.00 Matches: 243
Percent Similarity: 92.11% Conservative: 2
Best Local Similarity: 91.35% Mismatches: 19
Query Match: 48.50% Indels: 6
DB: 4 Gaps: 1

US-10-614-954-6 (1-451) x BI949616 (1-899)

QY 1 MetAlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyr 20
DB 110 ATGGCTTTCAAGATACAGCTCGACACCTCGCCAGCTACCGAGCTCTCTTCGATCTAC 169
QY 21 ThrGlnIleSerLeuLeuTyrProValSerAspSerGlnTyrProThrIleValSer 40
DB 170 ACCCAATCATGTCCTCTACCCCGTCTCTGATCTCTCAATATCCCACTATTGTGACG 229
QY 41 ThrPheGlnGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnVal 60
DB 230 ACCTTCAGCAGAGTCTTAAGCGCTTCTCCAGACCGCTCCATCGGTGCGAGCCGAGTTC 289
QY 61 LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp 80
DB 290 AAAGCCGAGGCGATTACGAGGGAACACAGGAACCTCTCTTCGTCCTCTTTTGAGGAC 349
QY 81 ValProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGly 100
DB 350 GTTCTCTCGTGTGTAGTGAAGACCTCCGCGATGATCTCTTCAGACCCACCGATCGAGGT 409
QY 101 MetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLys 120
DB 410 ATGGAAGAGGGGATACCTTATGGCGATGTTTGACGAGAACATCATCGGCCCAAGGAG 469

```

121 ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuGln 140
470 ACGTTACCTATTGGACCTGGTACTGTCGCCAGCACCACCAAGCCTGTATTTCTATTGCAG 529

141 LeuAsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAsp 160
530 CTCAACTTCATCAAGGCGGACTCATCTCTACTCTCCAGGCGTGCCTAACGCCCAATTC 649

161 MetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPhe 180
590 ATGGTAGCCAGATGCGGTGATCGTCTACTCTCCAGGCGTGCCTAACGCCCAATTC 649

181 ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrIleGlu 200
650 ACCGAAGAAGAAATGACGCGCATGAACTCGATCGCAAGAACGATAGTTCTTTACCTTGA- 708

201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAla-GlyCl 220
709 AACTATAGATTGGCCCCCGAGTAGATCATCATGATTGCAACCTGATGAGTCTGGTGG 768

220 YAspAlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAl 240
769 GTGACGCTGTCTCAGCGCGTCAGTGCAAGCTGGGGCGTCTTCACATTGACGCCAG-GC 827

240 aMetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSe 260
828 CATGTCAAGCTCAG-GATGCTGTACCAAGAACTCTGAGCATCAAC---AAAGTCGTGTC 883

260 rThrAspAlaLeu 265
884 -ACTGACGATGCTCTT 898

RESULT 2
LOCUS BI191800
DEFINITION library Fusarium sporotrichioides cDNA clone 12flifs 5', mRNA
sequence.
ACCESSION BI191800
VERSION BI191800.1 GI:14665479
KEYWORDS EST.
SOURCE Fusarium sporotrichioides
ORGANISM Fusarium sporotrichioides
REFERENCE 1 (bases 1 to 512)
AUTHORS Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A.,
Bersmand, M. and Roe, B.
ANALYSIS OF A Fusarium sporotrichioides EST database
UNPUBLISHED (2001)
OTHER ESTS: 12flifs.f1
CONTACT: Bruce A. Roe, University of Oklahoma, broe@ou.edu
DEPARTMENT OF Chemistry and Biochemistry
ADVANCED CENTER for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
TEL: 405 325 4912
FAX: 405 325 7762
EMAIL: broe@ou.edu
CONTACT DR. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
871 8e-94 gi|4379882|gb|AAD197 (AF121716)
trichothecena3-O-acetyltransfer
Seq primer: T3
High quality sequence stop: 476.
Location/Qualifiers
FEATURES
source
1. .512
/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="12flifs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"

/note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBlueScript; 3' end of cDNA cloned into XhoI site of pBlueScript"

ORIGIN

Alignment Scores: 1.4e-66 Length: 512
Pred. No.: 704.00 Matches: 131
Score: 704.00
Percent Similarity: 89.70% Conservative: 17
Best Local Similarity: 79.39% Mismatches: 17
Query Match: 30.16% Indels: 0
DB: 4 Gaps: 0

US-10-614-954-6 (1-451) x BI191800 (1-512)

QY 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21
Db 17 TCTTTTGACATAGAGCTCGACATCGCGCCAGAACCGCTCTTTTCAATCTACACC 76
QY 22 GlnIleSerLeuLeuTyrProValSerAspSerSertGlnTyrProThrIleValSerThr 41
Db 77 CAGATCAGTCTGCTTTACCCCGTCTCTGATCCCTCCAGTATCCACCATCGTCAGCAC 136
QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLys 61
Db 137 CTTGAGGAGGCTAAACCGCTCTCTCAACCTTCCCATGGTCCGGCCAGGTCAG 196
QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81
Db 197 ACCGAGGGCATCGGAGGAAACACAGAACTTCCAAGATCAATCCATATGAGGAGACA 256
QY 82 ProArgValValValLysAspLeuArgAspProSerAlaProThrIleGluGlyMet 101
Db 257 CCCGCTGTGTGTAAGACCTCCGTGATGATCTCTCAGCGCCACAGTCAGAGGGTTG 316
QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr 121
Db 317 AGAAGCGGGTTCGCCCTTAGAGATGTTTACGAGAAACGTCGCTCGAGGAGAGACA 376
QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141
Db 377 TTAGCTATCGGACTGGCAATGCCCCACGACGCCGAAGCCTGTGTGCTATTCGAGCTC 436
QY 142 AsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
Db 437 AACTTCATTAAAGCGGAGCTATCTTCACCGTCAACGGACACATGGTGTATGGACATG 496
QY 162 ValGlyGlnAspAla 166
Db 497 ACAGGACAGATGCT 511

RESULT 3

BI191865

LOCUS

DEFINITION BI191865 508 bp mRNA linear EST 10-JUL-2001
13b10fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone 13b10fs 5', mRNA
sequence.

ACCESSION

BI191865

VERSION

BI191865.1

KEYWORDS

GI:14665544

SOURCE

Fusarium sporotrichioides

ORGANISM

Fusarium sporotrichioides

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Mitosporic Hypocreales; Fusarium.

1 (bases 1 to 508)

Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A.,

Beremand, M. and Roe, B.

Analysis of a Fusarium sporotrichioides EST database

Unpublished (2001)

Other_ESTs: 13b10fs.fl

CONTACT: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Department of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability. Included
is the best homolog from a blastx search of Genbank nr 04-09-01
857 3e-92 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: T3
High quality sequence stop: 450.

FEATURES

source

1..508
Location/Qualifiers
/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="13b10fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBlueScript; 3' end of cDNA cloned into XhoI site of
pBlueScript"

ORIGIN

Alignment Scores:

Pred. No.: 1.72e-65 Length: 508
Score: 694.00 Matches: 129
Percent Similarity: 89.09% Conservative: 18
Best Local Similarity: 78.18% Mismatches: 18
Query Match: 29.73% Indels: 0
DB: 4 Gaps: 0

US-10-614-954-6 (1-451) x BI191865 (1-508)

QY 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21
Db 14 TCTTTTGACATAGAGCTCGACATCGCGCCAGAACCGCTCTTTTCAATCTACACC 73
QY 22 GlnIleSerLeuLeuTyrProValSerAspSerSertGlnTyrProThrIleValSerThr 41
Db 74 CAGATCAGTCTGCTTTACCCCGTCTCTGATCCCTCCAGTATCCACCATCGTCAGAC 133
QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLys 61
Db 134 CTTGAGGAGGCTAAACCGCTCTCTCAACCTTCCCATGGTCCGGCCAGGTCAG 193
QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81
Db 194 ACCGAGGGCATCGGAGGAGACACAGAACTTCCAAGATCAATCCATATGAGGAGACA 253
QY 82 ProArgValValValLysAspLeuArgAspProSerAlaProThrIleGluGlyMet 101
Db 254 CCCGCTGTGTGTAAGACCTCCGTGATGATCTCTCAGCGCCACAGTCAGAGGGTTG 313
QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr 121
Db 314 AGAAGCGGGTTCGCCCTTAGAGATGTTTACGAGAAACGTCGCTCGAGGAGACA 373
QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141
Db 374 TTAGCTATCGGACTGGCAATGCCCCACGACGCCGAAGCCTGTGTGCTATTCGAGCTC 433
QY 142 AsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
Db 434 AACTTCATTAAAGCGGAGCTATCTTCACCGTCAACGGACACATGGTGTATGGACATG 493
QY 162 ValGlyGlnAspAla 166
Db 494 ACAGGACAGATGCA 508

RESULT 4

```

BI200717          498 bp mRNA linear EST 10-JUL-2001
LOCUS             10le06fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION        library Fusarium sporotrichioides cDNA clone ole06fs 5', mRNA
sequence.
ACCESSION         BI200717.1 GI:14666689
VERSION           BI200717.1
KEYWORDS          Fusarium sporotrichioides
SOURCE            Fusarium sporotrichioides
ORGANISM          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                  Hypocreomycetidae; Hypocreales; Mitosporic Hypocreales; Fusarium.
REFERENCE         Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
                  Beremand,M. and Roe,B.
                  Analysis of a Fusarium sporotrichioides EST database
                  Unpublished (2001)
                  Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
                  Department of Chemistry and Biochemistry
                  Advanced Center for Genome Technology, University of Oklahoma
                  620 Parrington Oval, Norman, OK 73019, USA
                  Tel: 405 325 4912
                  Fax: 405 325 7762
                  Email: broe@ou.edu
                  Contact Dr. Marian Beremand regarding clone availability Included
                  is the best homolog from a blastx search of Genbank nr 04-09-01
                  743 8e-79 gi|4378882|gb|AAD197 (AF127176)
                  trichothecene3-O-acetyltransfer
                  Seq primer: T3
                  High quality sequence stop: 476.
FEATURES           source
                    1..498
                     /organism="Fusarium sporotrichioides"
                     /mol_type="mRNA"
                     /strain="Tri 10"
                     /db_xref="taxon:5514"
                     /clone="ole06fs"
                     /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
                     cDNA library"
                     /notes="Vector: pBluescript SK-; Site 1: EcoRI; Site_2:
                     XhoI; 5' end of cDNA cloned into EcoRI site of
                     pBluescript; 3' end of cDNA cloned into XhoI site of
                     pBluescript"
ORIGIN
Alignment Scores:
Pred. No.:        3,83e-63          Length:        498
Score:            672.50            Matches:       130
Percent Similarity: 86.75%          Conservative: 14
Best Local Similarity: 78.31%       Mismatches:    21
Query Match:      28.81%            Indels:        1
DB:               4                Gaps:          1

US-10-614-954-6 (1-451) x BI200717 (1-498)

QY 149 1leLeuThrValAsnGlyGlnHisGlyAlaMetAspMetValGlyGlnAspAlaValile 168
DB 3 ATTCTCACCGTCAACGACAAACATGTGCTATGACATGACAGGACAAAGATGCAATTATT 62
QY 169 ArgLeuLeuSerLysAlaCysArgAsnAspPropheThrGluGluGluMetThrAlaMet 188
DB 63 CGTCTTCTCTCAAGGCGTGCACCAACGAATCATTCACCGAGAGAGAAATCTCGGCCATG 122
QY 189 AsnLeuAspArgLysThrIleValProTyrLeuGluAsnTyrThrIleGlyProGluVal 208
DB 123 AACCTGATCGAAGACGGTAGTCCCTCTCTTGAAACTACAAAGTTGGTCTCTGAGCTA 182
QY 209 AspHisGlnIleValLysAlaAspValAlaGlyGlyAspAlaValLeuThrProValSer 228
DB 183 GACCACCAAGATGCCAAACCTGCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 239
QY 229 AlaSerTrpAlaPheThrPheSerProLysAlaMetSerGluLeuLysAspAlaAla 248

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DB 240 GCAAGCTGGCGCTTTCTTTTCATTCATCCCAAGGCCCTCTCGAGCTGAAACACGACGC 299
QY 249 ThrLysThrLeuAspAlaSerThrLysPheValSerThrAspAspAlaLeuSerAlaPhe 268
DB 300 ACAAGAGACTCTTGACGCGTCCGTCGAAGTTTGTGTCAACTGATGATGCTCTTTTCGGCGTTT 359
QY 269 IleTrpLysSerAlaSerArgValArgLeuGluArgIleAspGlySerAlaProThrGlu 288
DB 360 ATCTGGCAATCAACCTCGCGGTACGTCTCGCAGATTGGATGCTTCCACACTACTGAA 419
QY 289 PheCysArgAlaValAspAlaArgProAlaMetGlyValSerAsnAsnTyrProGlyLeu 308
DB 420 TTCTCCGCGCTGTGCATGCGGGCCCAATGGCGGTATCAAGCACATACCAGGCCTT 479
QY 309 LeuGlnAsnMetThrTyr 314
DB 480 CTTCAAAACATGACCTAC 497

RESULT 5
LOCUS    BI947129
DEFINITION
          BI947129.1 GI:16286403
          HVSME10003N10f Hordeum vulgare spike EST library HVcDNA0012
          (Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone
          HVSME10003N10f, mRNA sequence.
ACCESSION
          BI947129
          BI947129.1
VERSION
          BI947129
KEYWORDS
          Hordeum vulgare subsp. vulgare
SOURCE
          Hordeum vulgare subsp. vulgare
ORGANISM
          Hordeum vulgare subsp. vulgare
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Pooideae; Triticeae; Hordeum.
          1 (bases 1 to 1055)
          Wing,R., Muehlbauer,G.J., Close,T.J., Kleinhofs,A., Wise,R.,
          Heinen,S., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M.,
          Rambo,T., Simmons,J., Fenton,R.D., Malatrasi,M., Choi,D.W.,
          Gates,R. and Main,D.
          Development of a genetically and physically anchored EST resource
          for barley genomics: Fusarium infected Morex spike cDNA library
          Unpublished (2001)
          Contact: Wing RA
          Clemson University Genomics Institute
          Clemson University
          100 Jordan Hall, Clemson, SC 29634, USA
          Tel: 864 656 7288
          Fax: 864 656 4293
          Email: rwing@clemson.edu
          Total hg bases = 147
          Seq primer: AATTAACTCTCACTAAAGG
          High quality sequence start: 5
          High quality sequence stop: 668.
FEATURES           source
                    1..1055
                     /organism="Hordeum vulgare subsp. vulgare"
                     /mol_type="mRNA"
                     /cultivar="Morex"
                     /sub_species="vulgare"
                     /db_xref="taxon:112509"
                     /clone="HVSME10003N10f"
                     /tissue_type="Spike"
                     /lab_host="TJCI21"
                     /clone_lib="Hordeum vulgare spike EST library HVcDNA0012
                     (Fusarium infected)"
                     /notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site_2:
                     XhoI; Plants were grown at the University of Minnesota in
                     the GJ Muehlbauer lab; spikes were harvested and snap
                     frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium
                     graminearum inoculation (Heinen). In the TJ close lab at
                     the University of California, Riverside, total RNA was
                     prepared from each sample pool, equal quantities of all
                     eight RNA pools were combined, poly(A) RNA was purified
                     from the mixture, one primary unamplified cDNA library was
                     made, and 1 million pfu were in vivo excised to give

```



```

Db      258 TGGGCCAAGTGGGAGTCTCGGAGTATGACTTTGGGTTTGGACTGGGTAAAGCCTGAGAGT 199
QY      400 ValArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysPro 419
Db      198 GTGAGAGAGACTCGCTTGAACCTTTTGAGAGTTTGATGACCTTATGCCAAGAAGCCT 139
QY      420 AspGlyGluPheCysAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAla 439
Db      138 GATGGGAGTTTACGGCGCTCCATTCTCTGAGGAGTGGAGATATGAGAGACTAAAGGCG 79

QY      440 AspLysGluTrpThrLysTyrAlaGlnTyrValGly 451
Db      78 GATGAGAGTGGCAAAAGTACGCAAAAGTATATTGGG 43

RESULT 7
LOCUS   BI191864/c 481 bp mRNA linear EST 10-JUL-2001
DEFINITION
Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone 13b10fs 3', mRNA
sequence.
ACCESSION BI191864
VERSION BI191864.1 GI:14665543
KEYWORDS Fusarium sporotrichioides
SOURCE Fusarium sporotrichioides
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE 1 (bases 1 to 481)
AUTHORS Ren,Q., Tag,A., Pelpow,A., Lai,H., Kupfer,C., Peterson,A.,
Beremand,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Other ESTs: 13b10fs.r1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
745 4e-79 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: M13-20
High quality sequence stop: 340.
FEATURES
source
1. .481
/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="13b10fs"
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cDNA library"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"

ORIGIN
Alignment Scores:
Pred. No.: 2.54e-55 Length: 481
Score: 601.00 Matches: 110
Percent Similarity: 90.85% Conservative: 19
Best Local Similarity: 77.46% Mismatches: 13
Query Match: 25.75% Indels: 0
DB: 4 Gaps: 0

US-10-614-954-6 (1-451) x BI191864 (1-481)

QY      310 GlnAsnMetThrTyrHisSerThrIleGlyGluIleAlaAsnGluSerLeuGlyAla 329

```

```

Db      479 CAAAACATGACCTACCATGACTCGACCGTCGCCGGAATCGCAACGACCACTTGGCGCA 420
QY      330 ThrAlaSerArgLeuArgSerGluLeuAspProAlaSerMetArgGlnArgThrArgGly 349
Db      419 ACAGCATACAGCTGCGCTCGGAACCTCAACAGTGATCGTTTGGCGAGAGAACACAAAGCT 360
QY      350 LeuAlaThrTyrLeuHisAsnAsnProAspLysSerAsnValSerLeuThrAlaAspAla 369
Db      359 TTGGCGACGTACATGATGCGCTGCTGACAAAGTCGAGCGTCTCCCTGACCGCGGATGCG 300
QY      370 AspProSerThrSerValMetLeuSerSerTrpAlaLysValGlyLeuTrpAspTyrAsp 399
Db      299 AATCCGTCAGAGCAGCATCATGCTGAGTTCTCTGGCCCAAGGTGGGATGCTGGGATGAC 240
QY      390 PheGlyLeuGlyLeuLysProGluThrValArgAtgProIlePheGluProValGlu 409
Db      239 TTGGGTTTGGAGTGGGTAAAGCTGAGAGTGAGAGACCTCGCTTTCGAACTTTTGAG 180
QY      410 SerLeuMetTyrPheMetProLysLysProAspGlyGluPheCysAlaLeuSerLeu 429
Db      179 AGTTTGATGACTATTTATGCCCAAGACCTGATGGGAGCTTTACGGCGTCCATTTCTTTG 120
QY      430 ArgAspGluAspMetAspArgLeuLysAlaAspLysGluTrpThrLysTyrAlaGlnTyr 449
Db      119 AGGGATGAGGATATGAGAGACTAAAGGCGGATGAGGAGTGACAAAGTACGCAAGTAT 60
QY      450 ValGly 451
Db      59 ATTGGG 54

RESULT 8
LOCUS   BF253868
DEFINITION
546 bp mRNA linear EST 22-OCT-2001
HVSMEF0002F13f Hordeum vulgare seedling root EST library HVCNA0007
(Etiolated and unstressed) Hordeum vulgare subsp. vulgare cDNA
clone HVSMEF0002F13f, mRNA sequence.
ACCESSION BF253868
VERSION BF253868
KEYWORDS BF253868.2 GI:13116774
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 546)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
Yu,X., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W.,
Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex unstressed seedling root cDNA library
Unpublished (2001)
COMMENT On Nov 16, 2000 this sequence version replaced gi:11182973.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 376
Seq primer: AATAACCCCTCACTAAAGGG
High quality sequence stop: 532.
FEATURES
source
1. .546
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Morex"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HVSMEF0002F13f"
/tissue_type="Seedling root"
/lab_host="TJCl21"
/clone_lib="Hordeum vulgare seedling root EST library"

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HVCNDA0007 (Etiolated and unstressed)"
 /notes=vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
 Seeds were surface sterilized then germinated under axenic
 conditions in the dark at room temperature on filter paper
 with water, nystatin and cefotaxime in covered
 crystallization dishes. Five-day old seedling roots were
 then harvested, total RNA was prepared, poly(A) RNA was
 purified, one primary unamplified cDNA library was made,
 and 1 million pfu were in vivo excised to give pluescript
 SK(-) cDNA phagmids. These steps were performed in the TJ
 Close laboratory at the University of California,
 Riverside (Choi, Close, Penton). Phagemids were plated and
 picked at the Clemson University Genomics Institute (CUGI)
 (Segum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
 preparations, DNA sequencing and sequence analysis were
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,
 Oates, Rambo, Main). The sequence has been trimmed to
 remove vector sequence and contains a minimum of 100 bases
 of phred value 20 or above. For more details on library
 preparation and sequence analysis see
<http://www.genome.clemson.edu/projects/barley>. To order
 this clone see <http://www.genome.clemson.edu/orders> Also
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

ORIGIN

Alignment Scores:
 Pred. No.: 1,71e-52 Length: 546
 Score: 576.00 Matches: 105
 Percent Similarity: 79.43% Conservative: 34
 Best Local Similarity: 60.00% Mismatches: 34
 Query Match: 24.68% Indels: 2
 DB: 2 Gaps: 1

US-10-614-954-6 (1-451) x BF253868 (1-546)

QY 277 ArgLeuGluArgIleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArg 296
 DB 1 CGTCTTCCGTTGAGAGAAATCGGCCCGAAGCTCTATTCTGCGCGCCGTCGACGTCGA 60
 QY 297 ProAlaMetGlyValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsn 316
 DB 61 ACCAGCTTGATGTGCGCCAGGACTACCTCGGCAATCTCCAGAAATGCGCTACAGCAGT 120
 QY 317 SerThrIleGlyLeuIleAlaGluSerLeuGlyAlaThrAlaSerArgLeuArgSer 336
 DB 121 TCAACCTGTCTCAAAATAGCAATGAGCCCTTGGGTATTGTGGCCACTCGTCTACGAGCC 180
 QY 337 GluLeuAspProAlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsn 356
 DB 181 CAACTTGACCGCGAGTCTCTGCGACCTCGGACACAGCCCTTTGTTTCACATAGCTAA 240
 QY 357 AsnProAspGlySerAsnValSerLeuThrAlaAspAlaAspAlaProSerThrSerValMet 376
 DB 241 CATCCT- - - - -GGTACTTGTGTCTGTACAGCAGATGCCAATCCGCTACTGATATTATG 294
 QY 377 LeuSerSerTrpAlaValGlyLeuTyrAspTyrAspPheGlyLeuGlyValGly 396
 DB 295 TTGAGCTCTTGGGCCAAGACCGGATCGTGGAAATCATGACTTTGGTCTTGGGCTGGGAAAG 354
 QY 397 ProGluThrValArgArgProIlePheGluProValGluSerLeuMetTyrPheMetPro 416
 DB 355 CTGAGAGCGTAAGAGACCGATCTTTGAGCCTATGAGAGTTGATGATCTTATGCC 414
 QY 417 LysLysProAspGlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArg 436
 DB 415 AAGAGACCAAGATGAGAGAAATTAAGTCTGCTTGGCTTTGAGACGAGGATATGGAGATT 474
 QY 437 LeuLysAlaAspGlyGluTrpThrLysTyrAlaGlnTyrValGly 451
 DB 475 TTGAAGAGCGATGAGAAGTGGAGAAATTTGGACCGCTTCATCGGA 519

RESULT 9
 LOCUS
 DEFINITION

BI187781 411 bp mRNA linear EST 10-JUL-2001
 b2d04fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
 library Fusarium sporotrichioides cDNA clone b2d04fs 5', mRNA
 sequence.

ACCESSION BI187781
 VERSION BI187781.1 GI:14661460
 KEYWORDS EST.

SOURCE Fusarium sporotrichioides
 ORGANISM Fusarium sporotrichioides

REFERENCE 1 (bases 1 to 411)
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocremycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
 Beremand,M. and Roe,B.

TITLE Analysis of a Fusarium sporotrichioides EST database
 JOURNAL Unpublished (2001)

COMMENT Other ESTs: b2d04fs.f1

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability Included
 is the best homolog from a blastx search of Genbank nr 04-09-01

591 4e-61 gi|4378882|gb|AAD197 (AF121716)

trichothecenes-0-acetyltransfer

Seq primer: T3

High quality sequence stop: 307.

FEATURES

Location/Qualifiers
 1..411
 /organism="Fusarium sporotrichioides"
 /mol_type="mRNA"
 /strain="Tri 10"
 /db_xref="taxon:5514"
 /clone="b2d04fs"
 /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
 cDNA library"
 /note="vector: pBluescript SK-; Site1: EcoRI; Site_2:
 XhoI; 5' end of cDNA cloned into EcoRI site of
 pBluescript; 3' end of cDNA cloned into XhoI site of
 pBluescript"

ORIGIN

Alignment Scores:
 Pred. No.: 5,73e-52 Length: 411
 Score: 569.50 Matches: 110
 Percent Similarity: 89.78% Conservative: 13
 Best Local Similarity: 80.29% Mismatches: 13
 Query Match: 24.40% Indels: 1
 DB: 4 Gaps: 1

US-10-614-954-6 (1-451) x BI187781 (1-411)

QY 135 ProValIleLeuLeuGlnLeuAsnPhelIleYsGlyLeuIleuThrValAsnGly 154
 DB 3 CTGTGTTGCTATTGAGCTCAACTTCATTAGGCGGACTCATTTCTACCGTCAACGGA 62

QY 155 GlnHisGlyAlaMetAspMetValGlyGlnAspAlaValIleArgLeuLeuSerLysAla 174
 DB 63 CAACTGTTGCTATTGACATGACAGACAAGATGCAATTATTCTCTCTCCAGGCG 122

QY 175 CysArgAsnAspProPheThrGluGluMetThrAlaMetAsnLeuAspArgLysThr 194
 DB 123 TGCCGCAACGAATCATTTACCGAGGAGAAATCTCGGCCATGAACCTCGATCGCAGACG 182

QY 195 IleValProTyrLeuGluAsnTyrThrIleGlyProGluValAspHisGlnIleValLys 214
 DB 183 GTAGTCCCTCTCTCTTGAAGAACTACAAAGTTGGTCTGTAGCTAGACCCAGATCGCCAAA 242

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QY 215 AlaAspValAlaGlyAspAlaValLeuThrProValSerAlaSerTrpAlaPhePhe 234
Db 243 CTGGCGCTGGCT--GGCGACGCTCCACCCGACCGGCCAAGCAAGCTGGCGGTTCTTT 299
QY 235 ThrPheSerProlyAlaMetSerGluLeuLeuAspAlaAlaThrLysThrLeuAspAla 254
Db 300 TCATTACATCCCAAGGCCCTCTCGGAGCTGAAGACGACGCCACAAAGACTCTTGACGCG 359
QY 255 SerThrLysPheValSerThrAspAspAlaLeuSerAlaPheIleTrpLys 271
Db 360 TCGTCCAAGTTTGCTCACTGATGCTCTTCGGCGCTTTATCGGCAA 410

RESULT 10
BI201068/c
LOCUS BI201068.1 GI:14667040 448 bp mRNA linear EST 10-JUL-2001
DEFINITION o4c12fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
SOURCE library Fusarium sporotrichioides cDNA clone o4c12fs 3', mRNA
sequence.
ACCESSION BI201068
VERSION BI201068.1
KEYWORDS Fusarium sporotrichioides
SOURCE Fusarium sporotrichioides
ORGANISM Fusarium sporotrichioides
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
Beremand,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
694 4e-73 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: M13-20
High quality sequence stop: 303.
FEATURES
source
1..448
/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="o4c12fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"
ORIGIN
Alignment Scores: 2.55e-50 Length: 448
Pred. No.: 555.00 Matches: 102
Score: 90.23% Conservative: 18
Percent Similarity: 76.69% Mismatches: 13
Best Local Similarity: 23.78% Indels: 0
Query Match: 4 Gaps: 0
DB:

US-10-614-954-6 (1-451) x BI201068 (1-448)

QY 319 IleGlyGluLeuAlaAenGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeu 338
Db 447 GTGCCCGAAATCGCCACGAACCACTTGGCGACACAGCATCAGCGCTGGCGTGGAACTC 388

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QY 339 AspProLaserMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnPro 358
Db 387 AACAGTGATGCTTTGGCGCAGACGAACAAGCTTTGGCGAGTACATGCGATGGCGTGCCT 328
QY 359 AspLysSerAenValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSer 378
Db 327 GACAAGTCGACGCTCCCTGACCGCGATCGGAATCCGTCAAGCAGCATCATGCTGAGT 268
QY 379 SerTrpAlaLysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyProGlu 398
Db 267 TCCTGGGCCAAGTGGGATGCTGGAGATGACATTTGGTTGGTGGTGAAGCTGAG 208
QY 399 ThrValArgArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLys 418
Db 207 AGTGTGAGAAGACCTCGCTTTGAACCTTTTGAGAGTTTGATGTACTTTATATCCCAAGAAG 148
QY 419 ProAspGlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLys 438
Db 147 CTTGATGGGGAGTTTACGGCGTCCATTTCTCTGAGGAGTATGAGATATGAGAGACTAAG 88
QY 439 AlaAspLysGluTrpThrLysTyrAlaGlnTyrValGly 451
Db 87 GCGGATGAGGAGTGGCAAACTACGCAAGTATATTGGG 49

RESULT 11
BI192008
LOCUS BI192008.1 GI:14665687 514 bp mRNA linear EST 10-JUL-2001
DEFINITION l4c09fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
SOURCE library Fusarium sporotrichioides cDNA clone l4c09fs 5', mRNA
sequence.
ACCESSION BI192008
VERSION BI192008.1
KEYWORDS Fusarium sporotrichioides
SOURCE Fusarium sporotrichioides
ORGANISM Fusarium sporotrichioides
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
Beremand,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
730 3e-77 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: T3
High quality sequence stop: 476.
FEATURES
source
1..514
/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="l4c09fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"
ORIGIN
Alignment Scores: 1.84e-49 Length: 514
Pred. No.: 548.00 Matches: 101
Score:

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Percent Similarity: 87.97% Conservative: 16
 Best Local Similarity: 75.94% Mismatches: 16
 Query Match: 23.48% Indels: 0
 DB: 4 Gaps: 0

US-10-614-954-6 (1-451) x BI192008 (1-514)

QY 2 AlaPheLysLeuGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleThr 21
 DB 116 TCTTTTGCATAGAGTCGACATCATCGGCAGCAACCGCTCTTCTTTCAATCTACAC 175
 QY 22 GlnIleSerLeuLeuThrProValSerAspSerSerClnThrProThrIleValSerThr 41
 DB 176 CAGATCAGTCTCGTTTACCCCGCTCTGATCCCTCCAGATATCCACCATCGTCAGCAC 235
 QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61
 DB 236 CTGTGAGGAGCCCTTAAACGCTCTCTCAACCTTCCATGGGTGCGGCGCAGGTCAAG 295
 QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81
 DB 296 ACCGAGGCGCATCAGCGAAGGAAACACAGAGAACTTCCAAGATCATTCATATAGGAGACA 355
 QY 82 ProArgValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet 101
 DB 356 CCCCGCTCTGTGTGAAGACCTCCGTGATGATTCCTCAGCGCAACGATCGAGGGGTG 415
 QY 102 ArgLysAlaGlyThrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr 121
 DB 416 AGAAGGCGGTTTCCCTTAGAGATGTTGACAGAGACGTCGCTCGCAGGAAGACA 475
 QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLys 134
 DB 476 TTAGTATCGACCTGCAATGCGCCCAACGACCCGAAG 514

RESULT 12
 BI187780/c 457 bp mRNA linear EST 10-JUL-2001
 LOCUS b2d04fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
 DEFINITION library Fusarium sporotrichioides cDNA clone b2d04fs 3', mRNA
 sequence.

ACCESSION BI187780 GI:14661459
 VERSION BI187780
 KEYWORDS Fusarium sporotrichioides
 SOURCE Fusarium sporotrichioides
 ORGANISM Fusarium sporotrichioides
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 1 (bases 1 to 457)

REFERENCE Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
 Beremand,M. and Roe,B.
 Analysis of a Fusarium sporotrichioides EST database
 Unpublished (2001)
 COMMENT Other_ESTs: b2d04fs.r1
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu

FEATURES
 source
 1..457
 /organism="Fusarium sporotrichioides"
 /mol_type="mRNA"
 /strain="Tri 10"
 /db_xref="taxon:5514"

High quality sequence stop: 257.
 Location/Qualifiers
 1..457
 /organism="Fusarium sporotrichioides"
 /mol_type="mRNA"
 /strain="Tri 10"
 /db_xref="taxon:5514"

/clone="b2d04fs"

/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
 cDNA library"

/note="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2:
 XhoI; 5' end of cDNA cloned into EcoRI site of
 pBlueScript; 3' end of cDNA cloned into XhoI site of
 pBlueScript"

ORIGIN

Alignment Scores:
 Pred. No.: 5 44e-49 Length: 457
 Score: 543.00 Matches: 104
 Percent Similarity: 90.44% Conservative: 19
 Best Local Similarity: 76.47% Mismatches: 13
 Query Match: 23.26% Indels: 1
 DB: 4 Gaps: 0

US-10-614-954-6 (1-451) x BI187780 (1-457)

QY 316 AnSerThrIleGlyGluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArg 335
 DB 455 GACTCGACCGTCGCCGAATCGCAACGAACC-CTTGGGCGCAACAGCATCAGCGCTGCGC 397
 QY 336 SerGluLeuAspProAlaSerMetArgGlnArgThrArgGlyLeuAlaThrThrLeuHis 355
 DB 396 TCGGAACCTCAACAGTAGTGATCGTTTGGCGACGACGCAACAGCTTTGGCGACGTACATGCAT 337
 QY 356 AsnAsnProAspLysSerAsnValSerLeuThrAlaAspAlaAspProSerThrSerVal 375
 DB 336 GGCCTGCCCTGACAGCTGAGAGCTCTCCCTGACCGCCGATGCGAATCGCTCAGCAGCATC 277
 QY 376 MetLeuSerSerTrpAlaLysValGlyLeuTrpAspTrpAspPheGlyLeuGlyLeuGly 395
 DB 276 ATGCTGAGTTCCTGGGCAAGGTGGATGCTGGGAGTATGACTTTGGGTTTGGACTGGGT 217
 QY 396 LysProGluThrValArgArgProIlePheGluProValGluSerLeuMetThrPheMet 415
 DB 216 AAGCCTGAGAGGTGTGAGAGAGACCTCGCTTTGAAACCTTTTGAGAGTTTGATGTTTATG 157
 QY 416 ProLysLysProAspGlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAsp 435
 DB 156 CCCNAGAGCCTGATGGGAGTTTACGGGCTCCATTTCTCTGAGGATGAGGATATGGAG 97
 QY 436 ArgLeuLysAlaAspLysGluTrpThrLysTrpAlaGlnTrpValGly 451
 DB 96 AGACTAAAGCGCGATGAGGAGTGGACAAAGTACGCAAGTATATTGGG 49

RESULT 13

BI192452

LOCUS

DEFINITION

library Fusarium sporotrichioides cDNA clone m4b09fs 5', mRNA

sequence.

ACCESSION BI192452

VERSION BI192452.1

KEYWORDS

SOURCE

ORGANISM

Fusarium sporotrichioides

Fusarium sporotrichioides

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 1 (bases 1 to 392)

REFERENCE Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
 Beremand,M. and Roe,B.
 Analysis of a Fusarium sporotrichioides EST database
 Unpublished (2001)
 COMMENT Other_ESTs: m4b09fs.f1
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu

FEATURES

source

1..392

/organism="Fusarium sporotrichioides"

/mol_type="mRNA"

/strain="Tri 10"

/db_xref="taxon:5514"

Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
557 3e-57 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: T3
High quality sequence stop: 361.

FEATURES

source
1. .392
/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"

ORIGIN

Alignment Scores:
Pred. No.: 1.02e-47 Length: 392
Score: 530.50 Matches: 102
Percent Similarity: 87.02% Conservative: 12
Best Local Similarity: 77.86% Mismatches: 16
Query Match: 22.73% Indels: 1
DB: 4 Gaps: 1

US-10-614-954-6 (1-451) x BI192452 (1-392)

Qy 117 AlaProArgLysThrLeuProIleGlyProGlyThrGlyProAspProLysProVal 136
Db 3 GCTCCGAGGAGACATTAGCTATCGGACCTGGCAATGGCCCCAACGCCGAGCTGTG 62
Qy 137 IleLeuLeuGlnLeuAenPheIleLysGlyGlyLeuIleLeuThrValAenGlyGlnHis 156
Db 63 TTGCTATTGAGCTCACTTCAATTAAGGGCGGACTATTCTCACCCTCAACGGACAACAT 122
Qy 157 GlyAlaMetAspMetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArg 176
Db 123 GGTCTATTGACATGACAGACAGATGCAATTATTCGTTCTCTCAAGGGGTGCCG 182
Qy 177 AsnAspProPheThrGluGluMetThrAlaMetAsnLeuAspArgLysThrIleVal 196
Db 183 AACGATATTTCACCGAGGAGGAATCTCGGCCATGAACCTCGATCGCAAGACGGTAGTC 242
Qy 197 ProTyrLeuGluAenTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAsp 216
Db 243 CCTCTCTGAAAACTACAAAGTTGGTCCTGAGCTATACCACCAGATCGCCAAACCTGG 302
Qy 217 ValAlaGlyGlyAspAlaValLeuThrProValSerAlaSerTrpAlaPheThrPhe 236
Db 303 CCTGCT--GCGCAGCTCTCAACCGCACCGGCCCAAGCAAGCTGGGCGTCTTTTCATTC 359
Qy 237 SerProLysAlaMetSerGluLeuLysAspAla 247
Db 360 ACTCCAGGCGCTCTCGAGCTGAAAGAGCA 392

RESULT 14
BI191997
LOCUS
DEFINITION
518 bp mRNA linear EST 10-JUL-2001
14b10fs.xi Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone 14b10fs 5', mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
BI191997
GI:14665676
EST.
Fusarium sporotrichioides
Fusarium sporotrichioides
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 518)

AUTHORS

Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
Beremand,M. and Roe,B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
712 3e-75 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransfer

Seq primer: T3
High quality sequence stop: 484.

FEATURES

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ORIGIN

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Query Match: 22.71% Indels: 0
DB: 4 Gaps: 0

US-10-614-954-6 (1-451) x BI191997 (1-518)

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Qy 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81
Db 307 ACCGAGGCGATTCAGCGAGGAACACAGGAATCTTCCAGATCATTCATATGAGGAGACA 366
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Db 367 CCCCGTCTTGGTGAAGACCTCCGTGATGATTCTCAGCGCCCAACGATCGAGGGGTG 426
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Db 487 TTAGCTATCGGACCTGGCAATGGCCCAAC 516

RESULT 15
BI192498/c
LOCUS
BI192498
423 bp mRNA linear EST 10-JUL-2001

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 24, 2005, 05:23:41 ; Search time 126 Seconds
(without alignments)
2544.173 Million cell updates/sec

Title: US-10-614-954-6

Perfect score: 2334

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Fgapop 10.0 , Fgapext 0.5

Delop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Issued Patents NA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	1860.5	79.7	12949	3	US-09-538-414-11
6	1860.5	79.7	12949	4	US-10-074-279-11
7	1860.5	79.7	13737	3	US-09-538-414-10
8	1860.5	79.7	13737	4	US-10-074-279-10
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28	104	4.5	908	3	US-09-457-046B-23	Sequence 23, Appl
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31	102	4.4	16836	3	US-09-147-236-1	Sequence 1, Appli
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ALIGNMENTS

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US-09-538-414-5
; Sequence 5, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Salmeron, J.
; APPLICANT: Hohn, T.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Fusarium graminearum
US-09-538-414-5

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Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-614-954-6 (1-451) x US-09-538-414-5 (1-1356)

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QY 181 ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGln 200
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QY 201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly 220
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RESULT 2

US-10-074-279-5
; Sequence 5, Application US/10074279
; Patent No. 6646184
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Fusarium graminearum
US-10-074-279-5

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Pred. No.: 1,54e-257 Length: 1356
Score: 2334.00 Matches: 451
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-614-954-6 (1-451) x US-10-074-279-5 (1-1356)

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QY 41 ThrPheGluGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnVal 60
Db 121 ACCTTCGAGCAAGGTCTTAAAGCGCTTCTCGAAGCGCTCCCATGGTTCGACGGCCAGGTC 180
QY 61 LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp 80
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QY 381 AlaLysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLysProGluThrVal 400
DB 1141 GCCAAGGTGGACTCTGGGATTAAGACTTTGGCTCGGCTCGGTTAAGCCCGAGACTGTG 1200
QY 401 ArgArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAsp 420
DB 1201 AGACGCCCAATCTTTGAGCCTGTTGAGAGCTTGATGTACTTTATGCCAAGAGCCTGAT 1260
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DB 1261 GCGGAGTCTTGTGCGCGCTTCTCTGAGGAGATGAGGATATGACCGATTGAAGGCGGAT 1320
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RESULT 3

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US-09-538-414-1
; Sequence 1, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Fusarium sporotrichioides
US-09-538-414-1
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US-10-614-954-6 (1-451) x US-09-538-414-1 (1-1403)

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QY 22 GlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThr 41
DB 97 CAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCAGTATCCCCACCATCGTCAGACC 156
QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61
DB 157 CTTGAGGAAGGCTTAAACGCTCTCTCAAACTTCCCATGGGTCCGGCCAGGTCAAG 216
QY 62 AlaGluGlyIleSerGlyLysThrGlyThrSerPheIleValProPheGluAspVal 81
DB 217 ACCGAGGCGATCAGCGAAGAAACACAGAACTTCCAAGATCATTCATATGAGGAGACA 276
QY 82 ProArgValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet 101
DB 277 CCCCCTGTTGTTGGTGAAGACCTCCGTGATGATTTCTCAGCGCCCAACGATCGAGGGGTG 336
QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr 121
DB 337 AGAAAGCGGGTTCCTCCCTTAGAGATGTTTGAAGAACTGTCGCTCCGAGGAAGACA 396
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DB 457 AACTTCATTAAAGGCGGACTCATTTCTCAGCTCAACGGCAACATCGTGTGTATGGACATG 516
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QY 202 TyrThrIleGlyProGluValAspHisGlnIleValIysAlaAspValAlaGlyGlyAsp 221
Db 637 TACAAAGTTGGTCTGAGCTAGACACACAGATCGCAAACTCGCGCTGCT---GGCGAC 693

QY 222 AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet 241
Db 694 GCTCCACCCGACCGGCAAGGCAAGCTGGCGCTCTTTTCAATTCATCTCCCAAGGCCCTC 753

QY 242 SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261
Db 754 TCGAGCTGAAGACGAGCAGCAAGACTCTTGACGCGTCCCAAGTTTGTGCAACT 813

QY 262 AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle 281
Db 814 GATGATGCTCTTTTCGGGTTTATCTGGCAATCAACCTCGCGGTACGTCTCGCAAGATTG 873

QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301
Db 874 GATGCTTCCACACTACTGAATTTCTCGCGCTGTGACATGCGGGGCCCAATGGCGGTA 933

QY 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321
Db 934 TCAAGCACATACCCAGGCTCTTTCAAACATGACCTACCATGACTCGACCGTGGCGGAA 993

QY 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341
Db 994 ATCGCAACGAACCACTTGGCGCAACAGCATACAGCTCGCTCGGAACCTCAACAGTGAT 1053

QY 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnProAspLysSer 361
Db 1054 CGTTTCGCGACAGCAACAAAGCTTTGGCGACGTATACATGCTGGCTGCTGACAAAGTCG 1113

QY 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381
Db 1114 AGCGTCTCCCTGACCCGCGATGCGAATCCGTCAAGCAGCATCATGCTGAGTTCTCGGCC 1173

QY 382 LysValGlyLeuThrAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg 401
Db 1174 AAGGTGGGATGCTGGGAGTATGACTTTGGTTTGGACTGGGTAAGCTCGAGAGTGTGAGA 1233

QY 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
Db 1234 AGACCTCGCTTTGAACCTTTTGAGAGTTTCAATGATCTTTATGCCCCAAGAGCCTGTATGG 1293

QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspAspLeuLysAlaAspLys 441
Db 1294 GAGTTTACGGCGTCCATTCTCTGAGGGATGAGATATGGAGAGACTAAAGCGGATGAG 1353

QY 442 GluTrpThrLysTyrAlaGlnTyrValGly 451
Db 1354 GAGTGGACAAAGTACGCAAAAGTATATTGGG 1383

```

RESULT 4

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US-10-074-279-1
; Sequence 1, Application US/10074279
; Patent No. 6646184
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence18
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

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; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Fusarium sporotrichioides
US-10-074-279-1

Alignment Scores:
Pred. No.: 3,18e-203 Length: 1403
Score: 1860.50 Matches: 349
Percent Similarity: 88.67% Conservative: 50
Best Local Similarity: 77.56% Mismatches: 50
Query Match: 79.71% Indels: 1
DB: 4 Gaps: 1

US-10-614-954-6 (1-451) x US-10-074-279-1 (1-1403)

QY 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21
Db 37 TCTTTTGACATAGAGCTGACATCATCGGCCAGCAACCGCTCTTCTTTCAATCTACACC 96

QY 22 GlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThr 41
Db 97 CAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCAGTATCCCAACCATCGTCAGACC 156

QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61
Db 157 CTTGAGGAAGGCTAAACGCGCTCTCTCAACCTTCCCATGGGTGCGGGCCAGGTCAAG 216

QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81
Db 217 ACCGAGGGCATCAGGGAAGGAACAGAACTTCCAAAGTCAATCCATATGAGGAGACA 276

QY 82 ProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet 101
Db 277 CCCCCTCTTGTGTGAAGACCTCCGTGATGATTCTCAGCGCCCAACGATCCAGGGTTG 336

QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThr 121
Db 337 AGAAAGGCGGGTTCCCTTAGAGATGTTGACGAGAAAGCTCGTGGTCCGAGGAAGACA 396

QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141
Db 397 TTAGCTATCGGACCTGGCAATGCCCCCAACGACCCGAGCCCTGTGTGTTATGAGCTC 456

QY 142 AsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
Db 457 AACTTCATTAAAGGCGGACTCATTCTCACCGTCAACGAGCAACATGGTGTATGACATG 516

QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr 181
Db 517 ACAGGACAAGATGCAATTATTCTCTCTCAAGGGGTGCGGCAACGAATCATTCACC 576

QY 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAan 201
Db 577 GAGGAGGAATCTCGGCCATGAACCTCGATCCAAAGCGGTAGTCCCTCTCTCTTGAANAAC 636

QY 202 TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAsp 221
Db 637 TACAAAGTTGGTCTGAGCTAGACACCAAGTCCGCAACCTCGCGCTGCT---GGCGAC 693

QY 222 AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet 241
Db 694 GCTCCACCCGACCGGCAAGGCAAGCTGGCGCTCTTTTCAATTCATCTCCCAAGGCCCTC 753

QY 242 SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261
Db 754 TCGAGCTGAAGACGAGCAGCAGCAAGACTCTTGACGCGTCCCAAGTTTGTGCAACT 813

QY 262 AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle 281
Db 814 GATGATGCTCTTTTCGGGTTTATCTGGCAATCAACCTCGCGGTACGTCTCGCAAGATTG 873

QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301

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Db 874 GATGCTTCCACACTACTGAATCTCGCGGCTGTGACATGTCGGGGCCCAATGGCGTA 933
QY 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321
Db 934 TCAAGCACATACCCAGGCTCTTCTCAAAACATGACCTACCATGACTCGACCGTGGCGAA 993
QY 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341
Db 994 ATCGCCAAAGAACCACTTGGCGCAACAGCATCAAGCTCGCTCGGAACCTCAACAGTGAT 1053
QY 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer 361
Db 1054 CGTTTCGGACGACGAACACAGCTTTGGCGACGTACATGATGGCTGCTGACAAAGTCG 1113
QY 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381
Db 1114 AGCGTCTCCTGACCGCGCATCGAATCCGTCAAGCAGCATCATGCTGAGTCTCTGGCC 1173
QY 382 LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg 401
Db 1174 AAGGTGGGATGCTGGGAGTATGACTTTGGGTTTGGACTGGTAAGCCTGAGAGTGTGAGA 1233
QY 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
Db 1234 AGACCTCGCTTTGAACCTTTTGAGAGTTTGATGATCTTTATGCCCCAAGACCTGATGG 1293
QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441
Db 1294 GAGTTTACGGCGTCCATTTCTTGAGGGATGAGGATATGAGAGACTAAAGCGGATGAG 1353
QY 442 GluTrpThrLysTyrAlaGlnTyrValGly 451
Db 1354 GAGTGACAAAGTACGCAAGTATATTGGG 1383

RESULT 5

US-09-538-414-11
; Sequence 11, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 12949
; TYPE: DNA
; ORGANISM: Plasmid
US-09-538-414-11

Alignment Scores:
Pred. No.: 1,22e-201 Length: 12949
Score: 1860.50 Matches: 349
Percent Similarity: 88.67% Conservative: 50
Best Local Similarity: 77.56% Mismatches: 50
Query Match: 79.71% Indels: 1
DB: 3 Gaps: 1

US-10-614-954-6 (1-451) x US-09-538-414-11 (1-12949)

QY 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21
Db 11282 TCTTTTGACATAGCTCGACATCATCGGCGACCAACCGGCTCTCTTCAATCTACACC 11341
QY 22 GlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThr 41

Db 11342 CAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCCATGATATCCCACTATCGTCACACC 11401
QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61
Db 11402 CTTGAGGAGGCTAAACCCCTCTCTCAACCTTCCCATGGTGGCGGCCAGGTCAG 11461
QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81
Db 11462 ACCGAGGGCATCAGCGAAGAAACACAGAACTTCCAAAGATCATTCATATGAGGACA 11521
QY 82 ProArgValValValLysAspLeuArgAspProSerAlaProThrIleGluGlyMet 101
Db 11522 CCCGCTTGTGTGAAGACCTTCGTGATGATTCCTCAGCGCAACGATCAGAGGGTTG 11581
QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr 121
Db 11582 AGAAGGCGGGTTTCCCTTAGAGATGTTTGACGAGAACGTGCTCGTCCGAGGAACA 11641
QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuGluLeu 141
Db 11642 TTAGCTATCGGACCTGGCAATGCCCAACGACCCGAAAGCTGTGTGCTATTGCGACTC 11701
QY 142 AsnPheIleLysGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
Db 11702 AACTTCATTAAAGGCGGACTCATTCACCGTCAACGGAACAACATGGTCTATGGACATG 11761
QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr 181
Db 11762 ACAGGACAGATGCAATATTCTCTTCTCCAGGCGTGGCGCAACGAATCATTCACC 11821
QY 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsn 201
Db 11822 GAGGAGGAATCTCGGCCATGAACCTCGATCGCAAGACGCTAGTCTCTCTCTGAAAAC 11881
QY 202 TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAsp 221
Db 11882 TACAAAGTTGGTCTGAGCTAGACCAACAGATCGCCAAACCTGCGCGCTGCT---GGCGAC 11938
QY 222 AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet 241
Db 11939 GTTCACCCGCGACCGGCCAAGGCAAGCTGGGGTCTTTTTCATCTACTCCCAAGGCCCTC 11998
QY 242 SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261
Db 11999 TCGGAGCTGAAAGCGCAGCCACAAAGACTCTTGACGCGCTCGTCCAAGTTTGTCAACT 12058
QY 262 AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle 281
Db 12059 GATGATGCTCTTTTCGGCGTTTATCTGGCAATCAACCTCGCGGTACGTCTCGCAAGATTG 12118
QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301
Db 12119 GATGCTTCACACCTACTGAATTCGCCGCGCTGTGACATGTCGGGGGCCCAATGGCGGTA 12178
QY 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321
Db 12179 TCAAGCACATACCCAGGCTCTTCTCAAAACATGACCTACCATGACTCGACCGTGGCGAA 12238
QY 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341
Db 12239 ATCGCCAAAGAACCACTTGGCGCAACAGCATCACGCTCGCTCGGNACTCAACAGTGAT 12298
QY 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer 361
Db 12299 CGTTTGGCGAGAGAACACAAGCTTTGGCGAGCATCATGATGGCTGCTGCAAGTCG 12358
QY 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381
Db 12359 AGCGTCTCCTGACCGCGCATGCGAATCGTCAAGCAGCATCATGCTGAGTCTCTGGGCC 12418
QY 382 LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg 401

Db 12419 AAGCTGGGAGTCTGGGAGTATGACTTTGGGTTTGGACTGGTAAGCCTGAGAGTGTGAGA 12478
QY 402 AtgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
Db 12479 AGACCTCGCTTTGAACCTTTTGAGAGTTTGATGACTTTATGCCCCAAGAGCCTGATGG 12538
QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441
Db 12539 GAGTTTACGGCGTCCATTTCTCTGAGGATGAGGATATGAGAGACTAAAGCGGATGAG 12598
QY 442 GluTrpThrLysTyrAlaGlnTyrValGly 451
Db 12599 GAGTGACAAAGTACGCAAAAGTATATTGGG 12628

RESULT 6

US-10-074-279-11

; Sequence 11, Application US/10074279

; Patent No. 6646184

; GENERAL INFORMATION:

; APPLICANT: Hohn, T.

; APPLICANT: Salmeron, J.

; APPLICANT: Peters, C.

; APPLICANT: Kendra, D.

; APPLICANT: Reinders, J.

; APPLICANT: Kuznia, R.

; APPLICANT: Dill-Mackey, R.

; TITLE OF INVENTION: Transgenic Plant and Methods

; FILE REFERENCE: sequencelist

; CURRENT APPLICATION NUMBER: US/10/074,279

; CURRENT FILING DATE: 2002-02-12

; PRIOR APPLICATION NUMBER: US/09/538,414

; PRIOR FILING DATE: 2000-03-29

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 11

; LENGTH: 12949

; TYPE: DNA

; ORGANISM: Plasmid

US-10-074-279-11

Alignment Scores:

Pred. No.:	1,22e-201	Length:	12949
Score:	1860.50	Matches:	349
Percent Similarity:	88.67%	Conservative:	50
Best Local Similarity:	77.56%	Mismatches:	50
Query Match:	79.71%	Indels:	1
DB:	4	Gaps:	1

US-10-614-954-6 (1-451) x US-10-074-279-11 (1-12949)

QY 2 AlaphLeuLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21
Db 11282 TCTTTGACATAGAGCTCGACATCATCGCGCAGCAACCGCCCTCTTCTTCAATCTACACC 11341
QY 22 GlnIleSerLeuLeuTyrProValSerAspSerGlnTyrProThrIleValSerThr 41
Db 11342 CAGATCAGTCTCGTTTACCGCGTCTCTGATCCCTCCAGTATCCCAACCATCGTCAGCACC 11401
QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61
Db 11402 CTTGAGGAAGGCCCTAAACCGCTCTCTCAACCTTCCCATGGGTCCGGCGCAGGTCAAG 11461
QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81
Db 11462 ACCGAGGGCATCAGCGAGGAACACAGGAACTTCCAAAGTCAATTCATATGAGGAGACA 11521
QY 82 ProArgValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet 101
Db 11522 CCCCGTCTTGTTGAGAAACCTCCGTGATGATTCCTCAGCGCAACGATCGAGGGGTG 11581
QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr 121
Db 11582 AGAAAGCGCGGTTTCCCTTTAGAGATGTTTGACGAGAACGTGCTCGCTCCGAGGAAGACA 11641

RESULT 7

US-09-538-414-10

; Sequence 10, Application US/09538414

; Patent No. 6346655

QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141
Db 11642 TTAGCTATCGGACCTGGCAATGGCCCAACGACCGAAGCCTGTGTGTTATTGACGCTC 11701
QY 142 AsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
Db 11702 AACTTCATTAAAGGGCGGACTCATTTCTACCGTCAACGGCAACATGGTCTATGGACATG 11761
QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr 181
Db 11762 ACAGGACAGATGCAATTATTGTTCTTCTCCAGGGCGTGGCGCAACGAATCATTCACC 11821
QY 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrIleGluLeu 201
Db 11822 GAGGAGGAATCTCGGCATGAACCTCGATCGCAAGACGTAGTCCTCTCTCTGAAAC 11881
QY 202 TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAsp 221
Db 11882 TACAAAGTTGGTCTGAGCTAGACCACCAAGTCCGCAACCTCGCGCTCTCT--GGCGAC 11938
QY 222 AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet 241
Db 11939 GCTCCACCGCACCGCCAGCAAGCTGGGCGTCTTTTCATTCACTCCCAAGGCCCTC 11998
QY 242 SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261
Db 11999 TCGGAGCTGAAAGACGCGACCAAAAGACTTTCAGCGCTCGTCCAAAGTTTGTCTCACT 12058
QY 262 AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle 281
Db 12059 GATGATGCTCTTTTCGGCGTTTATCTGGCAATCAACTCGCGGTACGTCGCCAAGATG 12118
QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301
Db 12119 GATGCTTCCACACTACTGGAATTCGCCGCTGTGACATCGCGGCCCAATGGCGTA 12178
QY 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321
Db 12179 TCAAGCACATACCCAGGCGCTTCTCAAAACATGACCTACCATGACTCGACCGCTCGCGAA 12238
QY 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341
Db 12239 ATCGCCAAAGAACCACTTGGCCCAACAGCATCACCGCTCGGAACTCAACAGTGTAT 12298
QY 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer 361
Db 12299 CGTTTGGCGAGACGACACAAAGCTTTGGCGAGTACATGCTGCGCTGCAAGTCTG 12358
QY 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381
Db 12359 AGCGTCTCCTGACCGCGATCGGAATCCGTCAAGCAGCATCATGCTGAGTTCTCTGGGCG 12418
QY 382 LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg 401
Db 12419 AAGGTGGGATGCTGGGAGTATGACTTTGGGTTGGAGTGGGAAGCCTGAGAGTGTGAGA 12478
QY 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
Db 12479 AGACCTCGCTTTGAACCTTTTGAGAGTTTGATGTTATGCTTATGCCCAAGAGCCTGATGG 12538
QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441
Db 12539 GAGTTTACGGCGTCCATTTCTCTGAGGATGAGGATATGAGAGACTAAAGCGGATGAG 12598
QY 442 GluTrpThrLysTyrAlaGlnTyrValGly 451
Db 12599 GAGTGACAAAGTACGCAAAAGTATATTGGG 12628


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; TYPE: DNA
; ORGANISM: Plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
US-10-074-279-10

Alignment Scores:
Pred. No.: 1,346-201 Length: 13737
Score: 1860.50 Matches: 349
Percent Similarity: 88.67% Conservative: 50
Best Local Similarity: 77.56% Mismatches: 50
Query Match: 79.71% Indels: 1
DB: 4 Gaps: 1

US-10-614-954-6 (1-451) x US-10-074-279-10 (1-13737)

QY 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleThr 21
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 51 TCCTTTGACATAGAGCTCGACATCATCGGCCAGCAACCGCCTCTCTTTTCAATCTACACC 110
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 22 GlnIleSerLeuLeuThrProValSerAspSerGlnThrProThrIleValSerThr 41
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 111 CAGATCAGTCTCGTTTACCCGCTCTGATCCCTCCAGTATCCCAACCATCGTCAGCAC 170
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 171 CTTGAGGAAGGCTTAAACGCCTCTCTCAACCTTCCCATGGTTCGCGGCCAGGTCAAG 230
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 AlaGluGlyIleSerGluGlyAenThrGlyThrSerPheIleValProPheGluAspVal 81
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 231 ACCGAGGAGCATCAGCGAAGAAACACAGGAACCTTCCCAAGATCATTCATGAGGAGACA 290
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 82 ProArgValValLysAspLeuArgAspProSerAlaProThrIleGluGlyMet 101
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 291 CCCCGTCTTGTGTGTAAGAACCTTCCGTGATGATCTCTCAGCGCCACGATCGAGGGTTG 350
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 102 ArgLysAlaGlyThrProMetAlaMetPheAspGluAsnIleLeuAlaProArgLysThr 121
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 351 AGAAGCGGGTTTCCCTTTAGAGATGTTTACGAGAACGTCGTCCTCCGAGGAAGACA 410
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuGlnLeu 141
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 411 TTAGCTATCGGACCTCGGACATGATGATGATGATGATGATGATGATGATGATGATGAT 470
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 142 AsnPheIleLysGlyLeuLeuLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 471 AACTTCATTAAAGCGGAGCTCATCTCATCGTCACGCAACGATGCTGCTATGACATG 530
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr 181
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 531 ACAGGACAAGATCAATATTATCTCTCTCTCCAGGCGTGCAGCAACGAATCATTCACC 590
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProThrLeuGluAsn 201
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 591 GAGGAGGAATATCTCGGCCATGAACCTCGATCGCAAGACGCTAGTCCCTCTCTCTGAAC 650
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 202 TyrThrIleGlyProGluLeuAspHisGlnIleValLysAlaAspValAlaGlyLysAsp 221
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 651 TACAAAGTTGGTCTGAGCTAGACCAACCATCGCAACCTCGCGCTGCT---GGCGAC 707
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 222 AlaValLeuThrProValSerAlaSerTrpAlaPheThrPheSerProLysAlaMet 241
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 708 GCTCCACCCGACCGGCAAGCAAGCTGGCGGTCTTTTCAATCACTCCCAAGGCCCTC 767
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 242 SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 768 TCGGAGCTGAAGACGAGCCACAAAGACTTTGACGCGCTGCTCAAGTTGTGCAACT 827
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 262 AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle 281
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 828 GATGATGCTCTTTCCGGGTTTATCTGGCAATCAACCTCGCGCTAGCTCTCGCAAGATTG 887
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

; FILE REFERENCE: sequence1
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-538-414-7

Alignment Scores:
Pred. No.: 3e-100 Length: 1425
Score: 962.50 Matches: 202
Percent Similarity: 62.86% Conservative: 84
Best Local Similarity: 44.40% Mismatches: 158
Query Match: 41.24% Indels: 11
DB: 3 Gaps: 8

US-10-614-954-6 (1-451) x US-09-538-414-7 (1-1425)

QY 6 GlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleThrGlnIleSerLeu 25
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 CAACTTGATATTTGGGCAACAACTTCGCTGCTATACAACTATACACTCAATATGCTCT 123
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 26 LeuTyrProValSerSerSerGlnTyrProThrIleValSerThrPheGluGlnGly 45
Db 124 ATCTACCGTGTACAGATCTTCTGCTCATGCCATCATCTAAATACCTTTAAACAAGAGGA 183
QY 46 LeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLysAlaGluGlyLe 65
Db 184 CTTGAACATTTGGCTAAATAATTTCCAGTGGCTAGCAGGAATGCTGTAATAGAGGTGCT 243
QY 66 SerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspValProArgVal 85
Db 244 GACGAAGGTAAACACTGGTACCTACAGAAATGTCCCGTCAGACAAAATTTCCA---CTTATC 300
QY 86 ValLysAspLeuArgAspProSerAlaProThrIleGluGlyMetArgLysAlaGly 105
Db 301 GTCCAAGATCTTCGAGAAGATCTGTTCGCCCAACAATGGATTCGCTTGAATAAGCTGAC 360
QY 106 TyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThrLeu---ProIle 124
Db 361 TTTCTCTATCTACATGTAGACGAAAGACTTTTGGCGCTGGCATGCTATCAATCCACCT 420
QY 125 GlyProGlyThrGly---ProAspAspProLysProValIleLeuLeuGlnLeuAsn 143
Db 421 GGAACACTATAGTATGGCGCCCAAGAGTGGCGCTGTATTTGCAGTTCGAAGCAAACTTT 480
QY 144 IleLysGlyGlyLeuLeuThrValAsnGlyGlnHisGlyAlaMetAspMetValGly 163
Db 481 ATCTCGCGCGCTGCTCTTAATATTGTTCGGCAGCACAAATATTATGGATATAACAGGA 540
QY 164 GlnAspAlaValIleArgLeuSerLysAlaCysArgAsnAspProPheThrGluGlu 183
Db 541 CAGGAAGTATCATCACTTGTCTCAATAAATCTTGCACCAAAACCTTTCTCTGATGAA 600
QY 184 GluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLysLeuGluAsnTyr 203
Db 601 GAACCTGCTCTTGAATAATAGATAAAGCAAACTCTATCTCTTTGTTGATGAA---ACT 657
QY 204 IleGlyProGluValAsp-----HisGlnIleValLysAla-----AspValAlaGly 219
Db 658 TGGGAACCCGACACACCGCTAGTTCATGAATAATAGTGGAAACCTCTAGAAATACAAGTGA 717
QY 220 GlyAspAlaValLeuThrProValSer---AlaSerTyrAlaPheThrPheSerPro 238
Db 718 GAGGAAGGAAGAACAGCTTGTCTTGGAACTTACTTGGCGCTTATGTTGAATTTCTGCT 777
QY 239 LysAlaMetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPhe 258
Db 778 ATCTCATTCAGAAATCTGAGGATTTTGGCAATGCAGACATGTACTTCTGCACAAATTT 837
QY 259 ValSerThrAspAspAlaLeuSerAlaPheIleTyrLysSerAlaSerArgValArgLeu 278
Db 838 GTCTCCACTGATGATATCGTCACTGTCTTTCATCTGGAAATCAGTTTCTCGAGCCCTTTA 897
QY 279 GluArgIleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAla 298
Db 898 TCTCGACTTAAACCCAGAAACGAATCAAATTTAGGCGGTGCTGTGATGTATGAAAACGG 957
QY 299 MetGlyValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrLysAsnSerThr 318
Db 958 CTAGGACTCCCCAAACGATATCAGGGTATTAGTCAACATGACCTTTTAATACAGGTTC 1017
QY 319 IleGlyGluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeu 338
Db 1018 CTGAAAAGCTTGGATCATAAAAGTTTGGCGCTTCTTGGCATCATCATGATTCGACGAAGCTA 1077
QY 339 AspProAla-----SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsn 356
Db 1078 GACCCCTAAAGTCTTCGATTGGCGCTATAATACATGCGCACTTCTGCTACGCTCTTACCGCA 1137
QY 357 AsnProAspLysSerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMet 376
Db 1138 TGCCCGGACAGACTAAGGTTCCTATACCTCAACCAATTGATACTTATCTGGAATATG 1197
QY 377 LeuSerSerTrpAlaLysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLys 396

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Db 1198 GTCAAGTTCGTGGCAAAAGTCAGCCTGTATGACGTTGATTCAATCTAGGCTTGGGAAG 1257
QY 397 ProGluThrValArgArgProIlePheGluProValGluSerLeuMetTyrPheMetPro 416
Db 1258 CCCAAGAGTGTACGAGCGCGGCTTCATTCCCTTGAGAGCCTAATATATTTATGCCT 1317
QY 417 LysLysProAspGlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArg 436
Db 1318 AGATCTCCAGAGGTGAATGTGGTTGCTCTTTGCTTAGAGATAAAGATTGGAGTGC 1377
QY 437 LeuLysAlaAspLysGluThrThrLysTyrAlaGlnTyrValGly 451
Db 1378 CTGAATGCGGATAAAGAATGGCAAAATTATGCTACATATAGGA 1422

RESULT 10
US-10-074-279-7
; Sequence 7, Application US/10074279
; Patent No. 6646184
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/10/074,279
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-074-279-7

Alignment Scores:
Pred. No.: 3e-100 Length: 1425
Score: 962.50 Matches: 202
Percent Similarity: 62.86% Conservative: 84
Best Local Similarity: 44.40% Mismatches: 158
Query Match: 41.24% Indels: 11
DB: 4 Gaps: 8

US-10-614-954-6 (1-451) x US-10-074-279-7 (1-1425)
QY 6 GlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThrGlnIleSerLeu 25
Db 64 CAACCTTGATATTTGGGACACAACTTCGCTATACAACTATACACTCAATATGCTCT 123
QY 26 LeuTyrProValSerSerSerGlnTyrProThrIleValSerThrPheGluGlnGly 45
Db 124 ATCTACCGTGTACAGATCTTCTGCTCATGCCATCATCTAAATACCTTTAAACAAGAGGA 183
QY 46 LeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLysAlaGluGlyLe 65
Db 184 CTTGAACATTTGGCTAAATAATTTCCAGTGGCTAGCAGGAATGCTGTAATAGAGGTGCT 243
QY 66 SerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspValProArgVal 85
Db 244 GACGAAGGTAAACACTGGTACCTACAGAAATGTCCCGTCAGACAAAATTTCCA---CTTATC 300
QY 86 ValLysAspLeuArgAspProSerAlaProThrIleGluGlyMetArgLysAlaGly 105
Db 301 GTCCAAGATCTTCGAGAAGATCTGTTCGCCCAACAATGGATTCGCTTGAATAAGCTGAC 360
QY 106 TyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThrLeu---ProIle 124

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Db 361 TTTCCTATCTACATGTGTAGACGAAAGAGACTTTTGGCGCTTGCATGACTATCAATCCACCT 420
QY 125 GlyProGlyThrGly---ProAspAspProLysProValIleLeuLeuGlnLeuAsnPhe 143
Db 421 GGAACACTATAGTATGGCCGCGCAGAGTGGCGCTGTATTTGCAGTTTCAAGCAAACTTT 480
QY 144 IleLysGlyGlyLeuLeuThrValAsnGlyGlnHisGlyAlaMetAspMetValGly 163
Db 481 ATCTCGCGCGCTCGTTAACTATTGTGGCGCAGCACAAATATTATGATATAACAGGA 540
QY 164 GlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThrGluGlu 183
Db 541 CAGGAAGATATCACTTGTCTCAATAATAGTGGCACCACAAACCTTTCTCTGATGAA 600
QY 184 GluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsnTyrThr 203
Db 601 GAATGCTCATTTGGAATATAGATAAAGCAAACTATCTTCTTTGTTGATGAA---ACT 557
QY 204 IleGlyProGluValAsp-----HisGlnIleValLysAla-----AspValAlaGly 219
Db 658 TGGGAACCCGACACCCAGCTAGTTTCATGAATAAGTGGAAACCTCTAGAAATACAAAGTGA 717
QY 220 GlyAspAlaValLeuThrProValSer---AlaSerTrpAlaPhePheThrPheSerPro 238
Db 718 GAGGAAAGGAACAGCTTGTCTTCGAACCTCTACTTGGGCTTATGTTGAATTTTCTGCT 777
QY 239 LysAlaMetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPhe 258
Db 778 ATCTCATGCAATCTGAGGATTTGGCAATCAGACATGATGACTTCTGGCACAAATTT 837
QY 259 ValSerThrAspAspAlaLeuAlaPheIleTrpLysSerAlaSerArgValArgLeu 278
Db 838 GTCTCCACTGATGATATCGTCACTGCTTTCATCTCGGAATCACTTCTCGAGCCGCTTAA 897
QY 279 GluArgIleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAla 298
Db 898 TCTCGACTTAAACAGGAAACGAAATCAAAATTTAGGGCGTGTCTGTGATGTTAGAAAACGG 957
QY 299 MetGlyValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTrpHisAsnSerThr 318
Db 958 CTAGGACTCCCGCAACGATATCCAGGGTTATAGTCAATGACCTTTTATACAGGTTCC 1017
QY 319 IleGlyGluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLysArgSerGluLeu 338
Db 1018 CTCGAAAGCTTGGATCATATAAAGTTGGGCGTCTTTCATCATCGAATTCGACGAAAGCTA 1077
QY 339 AspProAla-----SerMetArgGlnArgThrArgGlyLeuAlaThrTrpLeuHisAsn 356
Db 1078 GACCCCTAAAGTCTTCGATTGGCCTATAATACATGCGCACTTGCTACGCTCCTTAGCCGA 1137
QY 357 AsnProAspLysSerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMet 376
Db 1138 TGCCCGGACAGACTAAGGTTTCTATACCTCAACCAATGATATCTTGAATATG 1197
QY 377 LeuSerSerTrpAlaLysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuLys 396
Db 1198 GTCAATGTCGGGCAAAAGTCAGCTGTATGACGTTGATTTCAATCTAGGCTTGGGAAG 1257
QY 397 ProGluThrValArgArgProIlePheGluProValGluSerLeuMetTyrPheMetPro 416
Db 1258 CCAAGAGTGATAGCGCGCGCGCTTCAATTTCCCTTGGAGCGCTAATATATTTATGCT 1317
QY 417 LysLysProAspGlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArg 436
Db 1318 AGATCTCCAGAGTGAATGGTGGTGTCTTCTTGGCTTAGAGATAAAGATTTGGGAGTGC 1377
QY 437 LeuLysAlaAspLysGluTrpThrLysTyrAlaGlnTyrValGly 451
Db 1378 CTGAATCGGATAAAGAAATGGACAAATTTATGCTTACACATATAGGA 1422

RESULT 11

US-09-457-046B-55

; Sequence 55, Application US/09457046B

; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 1347
; TYPE: DNA
; ORGANISM: Taxus cuspidata
US-09-457-046B-55

Alignment Scores: 3,26e-06 Length: 1347
Pred. No.: 142.00 Matches: 84
Score: 35.45% Conservative: 61
Best Local Similarity: 20.54% Mismatches: 184
Query Match: 6.08% Indels: 80
DB: 3 Gaps: 16

US-10-614-954-6 (1-451) x US-09-457-046B-55 (1-1347)

QY 5 IleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThrGlnIleSer 24
Db 103 CTCGAGCTCTCCGCGTGGACAGACTGCCAGGATGAAGTTGTACTTTTAGCGCCGTC 162
QY 25 LeuLeuTyrProValSerAspSerGlnTyrProThrIleValSerThrPheGluGln 44
Db 163 TTAGTCTACAATGCCAGCTCTCAGTCCATTTTGGAAATCCTGCACAGATTATTCGCGAG 222
QY 45 GlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLysAlaGly 64
Db 223 GCTCTCTCAAGGTGTGCAGTATTATCCCGCTTTTGGCGGGGATCAGACAGAAAGAA 282
QY 65 IleSerGlu-----GlyAsnThrGlyThrSerPheIleValProPheGlu 79
Db 283 AATGAGGAAGTGAAGTGGAGTGCACAGGGAGGGTGGCTGTTCTGGAAGCCCTGGTC 342
QY 80 AspValProArgValValLysAspLeuArgAspAspProSerAlaProThrIleGlu 99
Db 343 GACAAATGATCTTTCAGTCTTGGAGATTG----- 372
QY 100 GlyMetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArg 119
Db 373 GATGCCCAAAATGCACTTTATGAGCAGTTGCTCTTT----- 408
QY 120 LysThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeu 139
Db 409 ---TCGCTTCG-----CCCAATATACAGGTTTCAGGACCTCCATCTCTGATTTCTCAG 459
QY 140 GlnLeuAsnPheIleLysGlyLeuLeuLeuThrValAsnGlyGlnHisGlyAlaMet 159
Db 460 GTAACTCGTTTTACGTGTGGAGGTTTGTGTGGAGTAGGTTTTCACCATGTTATATGC 519
QY 160 AspMetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAsp--- 178
Db 520 GACGACGAGGAGGAACCTCAATTTCTTCAAGCCCTAGCATATGCAAGGGAGGAGACT 579
QY 179 ---ProPheThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValPro 197
Db 580 AAGCCTTTAGTGAACCACTATGG-----AATAGAGAACTGATAAAGCCC 624
QY 198 -----TyrLeuGluAsnTyrThrIleGlyProGluValAspHisGlnIleVal 213
Db 625 GAAGATCTAATGCACCTCCAAATTTTCATAAGTTTGGT-----TTGATACGCCCACTCTA 678
QY 214 LysAlaAspValAlaGlyGlyAspAlaValLeuThrProValSerAlaSerTrpAlaPhe 233
Db 679 AAACCTTGAT-----GAAATTTGTCAAGCATCT 705


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Db 655 CCTTCAATTTGTTGAGAAATTTGTTCAA----- 681
QY 226 ProValSerAlaSerTrpAlaPheThrPheSerProLysAlaMetSerGluLeuLys 245
Db 682 -----ACATATTTTATAGATTTTGAGACCATAAATATATACAA 723
QY 246 AspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThrAspAlaLeu 265
Db 724 CAATCT-----CTTATGGAAGAATGTAAAGAAATTTGCTCTCAITCGAAGTTGCA 774
QY 266 SerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgileaspGlySerAla 285
Db 775 TCAGCAATCACTGG-----ATAGCAAGGACCAAGAGCTTTCAAATTCAGAAAGTGAG 828
QY 286 ProThrGluPheCysArgAlaValAspAlaAspProAlaMetGlyValSerAsnAsnTyr 305
Db 829 TAGCTGAAATCTCTTCGGAATGGACATGAGG-----NACTCATTT 870
QY 306 ProGlyLeuLeuGlnAsnMetThrTyrHisAsnSer-----ThrIleGlyGluLeAla 323
Db 871 AATCCCCCTCTTCCAAGCGGATACTATGGTAACCTCGATGGTACCGCATGTGCAGTGAT 930
QY 324 AsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSer-----GluLeuAsp 339
Db 931 AATGTTCAAGACCTCTTAAGTGATCTTTTGGCGTCTAATAGTATATAAGAAATCA 990
QY 340 ProAlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAsp 359
Db 991 AAGGCTCTTTAAATCATATTTCAAGTCAAGAGCTGTGGTG-----AAGCCATCT 1041
QY 360 LysSerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSer 379
Db 1042 GAATTGGATGTGAATATGAATCATGAA-----AACGTAGTTGCATTTGCTGAT 1089
QY 380 TrpAlaLysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLysProGluThr 399
Db 1090 TGGAGCCGATGGGATTTGATGAAGTGGATTTTGGTTGGGGAATCGGTGAGTGTAAAG 1149
QY 400 ValArgArgProIlePheGluProValGluSerLeuMet-----TyrPheMet----- 415
Db 1150 -----CCTGTGCACCAACAGTCTGCTAGCATGCAAAATATTTTCTTTTCCTA 1200
QY 416 -----ProLysLysProAspGly 421
Db 1201 AAACCTTCCAAGAACCAAGCCCGATGGA 1227
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RESULT 15

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US-09-457-046B-44
; Sequence 44, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Taxus cuspidata
US-09-457-046B-44
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Alignment Scores:
Pred. No.: 0.00667 Length: 1320
Score: 113.00 Matches: 93
Percent Similarity: 35.84% Conservative: 69
Best Local Similarity: 20.58% Mismatches: 186
Query Match: 4.84% Indels: 104
DB: 3 Gaps: 20
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US-10-614-954-6 (1-451) x US-09-457-046B-44 (1-1320)

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QY 5 IleGlnLeuAspThrIleuGlyGlnLeuProGlyLeuLeuSerIleTyrThrGlnIleSer 24
Db 82 CTGCAGCTCTCCACCGCTTGACAATCTACACGGGTGAGAGAAACACATTTTTTAACACCTTG 141
QY 25 LeuLeuTyrProValSerAspSer----- 32
Db 142 TTAGTCTTCAATGCCTCAGACAGAGTTTCCGTAGATCCTGCAAAAGTAATTCGGCAGGCT 201
QY 33 ---SerGlnTyrProThrIleValSerThrPheGluGlnGlyLeuLysArgPheSerGlu 51
Db 202 CTCTCAAGGTGTTGGTGACTACTATTCCTTTTGCAGGCGCTCTCAGAAAAAGAAAT 261
QY 52 AlaValProTrpValAlaGlyGlnValLysAlaGluGlyIleSerGluGlyAsnThrGly 71
Db 262 -----GGAGATCTTGAAGTGGAGTGCACAGGGGAG-----GCT 294
QY 72 ThrSerPheIleValProPheGluAspValProArgValValValLysAspLeuArgAsp 91
Db 295 GCTCTGTTTGTGGAAGCCATGGCTGACACTGACCTCTCAGTCTTTAGGAGATTTG----- 348
QY 92 AspProSerAlaProThrIleGlyMetArgLysAlaGlyTyrProMetAlaMetPhe 111
Db 349 GATGACTACAGTCCCTTCACTTGAGCACTA-----CTTTT 384
QY 112 AspGluAsnIleAlaProArgLysThrLeuProIleGlyProGlyThrGlyProAsp 131
Db 385 -----TGCTCTCCG-----CCTGATACAGATATTGAG 411
QY 132 AspProLysProValIleLeuLeuGlnLeuAsnPheIleLysGlyGlyLeuIleLeuThr 151
Db 412 GACATCCATCCCTCTGGTGGTTCAGGTAACCTGTTTACATGTGGAGGTTTGTGTAGGG 471
QY 152 ValAsnGlyGlnHisGlyAlaMetAspMetValGlyGlnAspAlaValIleArgLeuLeu 171
Db 472 GTGAGTTTCTGCATGTGTATATGTATGATGAGTAGGAGCGGCAGTCTTTATAGCCATG 531
QY 172 SerLysAlaCysArg-----AsnAspProPheThrGluGluMet 185
Db 532 CGAGAGATGGCAAGGGAGAGATTAAAGCCTCTCGAGCCAATATGGAAGAGAGAAATG 591
QY 186 ThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsnTyrThrIleGly 205
Db 592 CTGAAGCCGGAAGACCCCTTTATACCGTTTCCAGTATTATACCTTTCAATGATTGCCCG 651
QY 206 ProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAspAlaValLeuThr 225
Db 652 CCTTCAACATTCGGGAATAAGTTCAA-----GGATCTCTTGTATTAAACC 696
QY 226 ProValSerAlaSerTrpAlaPheThrPheSerProLysAlaMetSerGluLeuLys 245
Db 697 -----TCTGAGACAATA 708
QY 246 AspAlaAlaThrLysThrIleu-----AspAlaSerThrLysPheValSerThrAspAla 264
Db 709 AATGTGTATCAAAATGCTTAGGGAAGAAAGAAATTTTGTCTCGCTTCGAGTT 768
QY 265 LeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgileaspGlySer 284
Db 769 GTATCTGCATTGGCTGG-----ATAGCAAGCAAGGCTCTTCAAAATTCACATAGT 822
QY 285 AlaProThrGluPheCysArgAlaValAspAlaAspProAlaMetGlyValSerAsnAsn 304
Db 823 GAGAAATGTGAAGCTTATTTTTCATGAGATGAGAAATTTATTAAT----- 870
QY 305 TyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGluIle----- 322
Db 871 ---CCACCACCTTTCGAAGGGA-----TACTACGGTAATTTTGTGGTACCCTATGTGCA 921
QY 323 -----AlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuAspSerGluLeuAsp 339
Db 922 ATGGATATGTCAAGGACCTATTAAAGTGAATCTCTTTCGGTGTGTAGGATTATAAAG 981
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QY 340 ProAlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAsp 359
Db 982 AAAGCAAGGTCTCT-----TAAATGAGCATTTCACG 1014
QY 360 LysSerAsnValSerLeuThrAlaAspAlaAspProSerThrSer-----Val 375
Db 1015 TCAACAATCGTACACCCCGTCTCTGGATCAGATGAGAGTATCAATTATGAAAAACATAGTT 1074
QY 376 MetLeuSerSerTrpAlaLysValGlyLeuTrpAspTyrAspPheGlyLeuGly 395
Db 1075 GGATTTGGTGATCGAAGGCGATTGGGATTTGATGAAGTAGACTTTGGTGGGGCATGCA 1134
QY 396 LysProGluThrValArgProIlePheGluProValGluSerLeuMet---TyrPhe 414
Db 1135 GATAATGTAAGTCTCGTCAACATGGATTGAAGGATGTTTCAGTCGTCGCAAAAGTTATTTT 1194
QY 415 Met-----ProLys---LysProAspGly 421
Db 1195 CTTTCATAGACCTCCCAAGAATAACCCCGATGGA 1230
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Job time : 173 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 24, 2005, 07:55:19 ; Search time 768 Seconds
(without alignments)
3374.213 Million cell updates/sec

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Perfect score: 2334
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications NA -QWMT=fastac -SUFFIX=p2n.rnpb -MINMATCH=0.1
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Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2334	100.0	1356	16	US-10-614-954-5	Sequence 5, Appli
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4	1860.5	79.7	1403	16	US-10-614-954-1	Sequence 1, Appli
5	1860.5	79.7	12949	13	US-10-074-279-11	Sequence 11, Appli
6	1860.5	79.7	12949	16	US-10-614-954-11	Sequence 11, Appli
7	1860.5	79.7	13737	13	US-10-074-279-10	Sequence 10, Appli
8	1860.5	79.7	13737	16	US-10-614-954-10	Sequence 10, Appli
9	962.5	41.2	1425	13	US-10-074-279-7	Sequence 7, Appli
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23	158.5	6.8	5922	17	US-10-437-963-40613	Sequence 40613, A
24	158.5	6.8	1401	17	US-10-437-963-77069	Sequence 77069, A
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26	157.5	6.7	3424	16	US-10-424-599-118915	Sequence 118915,
27	157.5	6.7	1664	16	US-10-425-114-21511	Sequence 21511, A
28	155.5	6.7	1185	17	US-10-437-963-97623	Sequence 97623, A
29	155.5	6.6	1692	18	US-10-739-930-3680	Sequence 3680, Ap
30	153.5	6.6	1690	16	US-10-425-114-11942	Sequence 11942, A
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37	143	6.1	1428	9	US-09-938-842A-1390	Sequence 1390, Ap
38	143	6.1	1428	11	US-09-938-842A-1390	Sequence 1390, Ap
39	143	6.1	1451	17	US-10-437-963-6385	Sequence 6385, Ap
40	143	6.1	1765	16	US-10-424-599-134525	Sequence 134525,
41	142.5	6.1	1347	9	US-09-866-570A-55	Sequence 55, Appli
42	142	6.1	1347	9	US-09-866-570A-55	Sequence 55, Appli
43	142	6.1	1347	15	US-10-166-984-55	Sequence 55, Appli
44	142	6.1	1347	15	US-10-166-984-55	Sequence 55, Appli
45	142	6.1	1347	16	US-10-166-984-55	Sequence 55, Appli

ALIGNMENTS

RESULT 1
US-10-074-279-5
; Sequence 5, Application US/10074279
; Publication NO. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence1
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5

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; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Fusarium graminearum
US-10-074-279-5

Alignment Scores:
Pred. No.: 1.14e-267 Length: 1356
Score: 2334.00 Matches: 451
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

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QY 21 ThrGlnIleSerLeuLeuTyrProValSerAspSerGlnTyrProThrIleValSer 40
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QY 41 ThrPheGlnGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnVal 60
DB 121 ACCTTCGACGAGGTCTTAAGCGCTTCTCGAAGCGCTCCCATGGGTGCGCAGCCAGGTC 180
QY 61 LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp 80
DB 181 AAGCCGAGGGCAATTAGCGAGGAAACACAGGAACCTTCCTTTATCGTCTCTTTGAGGAC 240
QY 81 ValProArgValValValLysAspLeuArgAspProSerAlaProThrIleGluGly 100
DB 241 GTTCTCTGTGTGTAGTGAAGACCTCCGCGATGATCCTTCAGCGCCACGATCGAGGT 300
QY 101 MetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLys 120
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QY 121 ThrLeuProIleGlyProGlyThrGlyProAspProLysProValIleLeuLeuGln 140
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DB 481 ATGCTAGGCCAAGATGCGGTGATCCGCTACTCTCAAGCGCGTCCGTAACGACCCATT 540
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DB 541 ACCGAGAGGAATAGCGGCAATGACCTCGATCGCAAGCAGATAGTTCTTACCTTGA 600
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RESULT 2
US-10-614-954-5
; Sequence 5, Application US/10614954
; Publication NO. US20040034884A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/614,954
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Fusarium graminearum
US-10-614-954-5

Alignment Scores:
Pred. No.: 1.14e-267 Length: 1356
Score: 2334.00 Matches: 451
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

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QY 241 MetSerGluLeuLysAspAlaThrLysThrLeuAspAlaSerThrLysPheValSer 260
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QY 261 ThrAspAspAlaLeuSerAlaPheIleTyrLysSerAlaSerArgValArgLeuGluArg 280
DB 781 ACTGACGATGCTCTTTCGGGTTTCATCTGGAATCGGCCCTCTCGCGTGGTCTCGAAGA 840
QY 281 IleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGly 300
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QY 341 AlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLys 360
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QY 361 SerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrp 380
DB 1081 TCCAACGATATCCCTGACGGCTGATCGGACCCATCTACCAAGCGTCATGCTGAGTCTTGG 1140

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QY 421 GlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAsp 440
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DB 1321 AAGGAGTGGACCAAGTATGCGGATGACGTGTGGT 1353

RESULT 3
US-10-074-279-1
; Sequence 1, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Fusarium sporotrichioides
US-10-074-279-1

Alignment Scores:
Pred. No.: 3,46e-211 Length: 1403
Score: 1860.50 Matches: 349
Percent Similarity: 88.67% Conservative: 50
Best Local Similarity: 77.56% Mismatches: 50
Query Match: 79.71% Indels: 1
DB: 13 Gaps: 1

US-10-614-954-6 (1-451) x US-10-074-279-1 (1-1403)

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QY 22 GlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThr 41
DB 97 CAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCAGTATCCACCATCGTCAGCACC 156
QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61
DB 157 CTGAGGAAGGCTTAAAGCGCTCTCTCAACCTTCCATCGGTCGCGGCGAGGTCAAG 216
QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81
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QY 82 ProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet 101
DB 277 CCCCCTGTTGTTGTAAGACCTCCGTTGATGATTCCTCAGCGCCACGATCGAGGGGTG 336
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Db 337 AGAAGCGCGGTTTCCCTTAGAGATGTTTACGAGAACGTCGTCGCGAGGAAGACA 396
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Db 397 TTAGCTATCGGACCTGGCAATGGCCCAACGAGCCCGAAGCCTGTGTGTATTGCGACTC 456
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QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspPropheThr 181
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QY 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsn 201
Db 577 GAGGAGGAATCTCGGCCATGAACCTCGATCGCAACGCGTAGTCTCTCTTGAANAAC 636
QY 202 TyrThrIleGlyProGluValAspHisGlnIleValIysAlaAspValAlaGlyGlyAsp 221
Db 637 TACAAAGTTGGTCTCGAGCTAGACACCAACAGATCGCCAAACCTGCGGCTGCT---GGCGAC 693
QY 222 AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet 241
Db 694 GTCTCCACCGCACCGGCCAAGGCAAGCTGGCGCTTCTTTTCAATTCATCTCCCAAGGCGCTC 753
QY 242 SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261
Db 754 TCGGAGCTGAAGACCGCAGCCCAAGACTCTTGACGCGTGCCTCAAGTTTGTCACT 813
QY 262 AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle 281
Db 814 GATGATGCTCTTTTCGCGGTTTATCTGCAATCAACCTCGCGGTACGTCGCAAGATTG 873
QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301
Db 874 GATGCTTCCACACTACTGAATTTCTCGCGCTGTGACATGCGGGGCCCAATGGCGCTA 933
QY 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321
Db 934 TCAGCACATACCCAGCGCTTCTTCAAAACATGACCTACATGACCTCGACCGTGCAGG 993
QY 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341
Db 994 ATCGCCAACGAACCACTTGGCGCAACAGCATCACGCTCGGCTCGGAACCTCAACAGTGAT 1053
QY 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnProAspLysSer 361
Db 1054 CGTTTCGCGACGACACAAAGCTTTGGCGACGTATACATGCTGGCTGCTGACAAAGTCG 1113
QY 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381
Db 1114 AGCGTCTCCTGACCCCGATGGAAATCCGTCAAGCAGCATCATGCTGAGTTCTCTGGGC 1173
QY 382 LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg 401
Db 1174 AAGTGGGATGCTGGGAGTATGACTTTGGTTGGACTGGTAAAGCTCGAGAGTGTGAGA 1233
QY 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
Db 1234 AGACCTCGCTTGAACCTTTTGAGAGTTTGAAGTACTTTATGTCCTCAAGAGCCCTGATGGG 1293
QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441
Db 1294 GAGTTTACCGCGTCCATTTCTCTGAGGGATGAGATATGAGAGACTAAAGCGGATGAG 1353
QY 442 GluTrpThrLysTyrAlaGlnTyrValGly 451
Db 1354 GAGTGACAAAGTACGCAAGTATATTGGG 1383

RESULT 4

US-10-614-954-1

/ Sequence 1, Application US/10614954
/ Publication No. US20040034884A1
/ GENERAL INFORMATION:
/ APPLICANT: Hohn, T.
/ APPLICANT: Salmeron, J.
/ APPLICANT: Peters, C.
/ APPLICANT: Kendra, D.
/ APPLICANT: Reinders, J.
/ APPLICANT: Kuznia, R.
/ APPLICANT: Dill-Mackey, R.
/ TITLE OF INVENTION: Transgenic Plant and Methods
/ FILE REFERENCE: sequence list
/ CURRENT APPLICATION NUMBER: US/10/614,954
/ CURRENT FILING DATE: 2003-07-07
/ PRIOR APPLICATION NUMBER: US/09/538,414
/ PRIOR FILING DATE: 2000-03-29
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 1403
/ TYPE: DNA
/ ORGANISM: Fusarium sporotrichioides
US-10-614-954-1

Alignment Scores:

Pred. No.: 3,46e-211 Length: 1403
Score: 1860.50 Matches: 349
Percent Similarity: 88.67% Conservative: 50
Best Local Similarity: 77.56% Mismatches: 50
Query Match: 79.71% Indels: 1
DB: 16 Gaps: 1

US-10-614-954-6 (1-451) x US-10-614-954-1 (1-1403)

QY 2 AlaPheLysIleGleLeuAspThrLeuGlyGlnLeuProGlyLeuSerIleTyrThr 21
Db 37 TCTTTTGACATAGAGCTCGACATCATCGGCCAGCAACCGCCTCTCTTTCAATCTACACC 96
QY 22 GlnIleSerLeuLeuTyrProValSerSerSerGlnTyrProThrIleValSerThr 41
Db 97 CAGATCAGTCTCGTTTACCCCTCTCTGATCCCTCCAGTATCCCAACCATCGTCAGCACC 156
QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61
Db 157 CTTGAGGAGGCTAAACGCTCTCTCAACCTTCCATCGGTGCGCGCCAGGTCAAG 216
QY 62 AlaGluGlyIleSerGluLysAsnThrGlyThrSerPheIleValProPheGluAspVal 81
Db 217 ACCGAGGGCATCAGCGAAGAAACACAGAACTTCCAAGATCATTCATATGAGGAGACA 276
QY 82 ProArgValValLysAspLeuArgAspProSerAlaProThrIleGluGlyMet 101
Db 277 CCGGCTTGTGTGTAAGACCTCGGTGATGATTCCTCAGCGCCCAACGATCGAGGGGTG 336
QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThr 121
Db 337 AGAAAGCGGGTTTCCCTTAGAGATGTTTGACGAGAACGTCGTCGCTCCGAGGAGACA 396
QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141
Db 397 TTAGCTATCGGACCTGGCAATGGCCCAACGAGCCCGTGTGTGTATTGCGACTC 456
QY 142 AsnPhelileysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
Db 457 AACTTCATTAAAGGCGGACTCACTTCACCGTCAACGGACAACATGGTGCTATGGACATG 516
QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspPropheThr 181
Db 517 ACAGGACAAGATCAATATTCTCTCTCCAAAGCGTGGCCGCAACGAATCATTCACC 576
QY 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsn 201
Db 577 GAGGAGGAATCTCGGCCATGAACCTCGATCGCAACGCGTAGTCTCTCTTGAANAAC 636

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QY 202 TyrThrIleGlyProGluValAspHisGlnIleValIysAlaAspValAlaGlyGlyAsp 221
Db 637 TACAAAGTTGGTCTCGAGCTAGACCAACAGATCGCCAAACCTCGCTGCT--GGCGAC 693
QY 222 AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProIysAlaMet 241
Db 694 GCTCCACCGCCAGCCGCAAGCAAGCTGGGCGCTTTTTCATTCATCTCCCAAGGCCCTC 753
QY 242 SerGluLeuLysAspAlaAlaThrIysThrLeuAspAlaSerThrIysPheValSerThr 261
Db 754 TCGAGCTGAAAGACGAGCCACCAAGAGCTCTTGACGGCTGCTCCAAAGTTTGTCTCACT 813
QY 262 AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle 281
Db 814 GATGATGCTCTTTCGGCGTTTATCTGGCAATCAACCTCGCGCTAGCTCTCGCAAGATTG 873
QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301
Db 874 GATGCTTCCACACCTACTGAATTTCTCGCGCTGTGTGACATGCGGGGCCCAATGGGCGTA 933
QY 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321
Db 934 TCAAGCACATACCAGGCCCTTCTTCAAACATGACCTACCATGACCTGACCGTGGCGGAA 993
QY 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341
Db 994 ATCGCCAAACGACCACTTGGCGCAACAGCATCAGCGCTGCGCTCGGAACCTCAACAGTGAT 1053
QY 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer 361
Db 1054 CGTTTGGCAGACGAAACACAAAGCTTTGGCGACGTACATGATGCGCTCGCTGCAAGTCG 1113
QY 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381
Db 1114 AGCGTCTCCCTGACCGCGGATGGATCCGATCCGTCAGCAGCATCATGCTGAGTTCTGGGCC 1173
QY 382 LysValGlyLeuThrAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg 401
Db 1174 AAGGTGGGATGCTGGGAGTATGACTTTGGTGGTAAAGCTGAGAGTGTGAGA 1233
QY 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
Db 1234 AGACCTCGCTTTGAACCTTTGAGAGTTTGTATGATCTTTATGATGATGATGATGATGAT 1293
QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441
Db 1294 GAGTTTACGGCGTCCATTTCTTGAGGGATGAGGATATGAGAGACTAAAGCGCGATGAG 1353
QY 442 GluTrpThrLysTyrAlaGlnTyrValGly 451
Db 1354 GAGTGGCAAAAGTACGCAAGTATATTGGG 1383
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RESULT 5

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US-10-074-279-11
; Sequence 11, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 11
; LENGTH: 12949
; TYPE: DNA
; ORGANISM: Plasmid
US-10-074-279-11

Alignment Scores:
Pred. No.: 1,03e-209 Length: 12949
Score: 1860.50 Matches: 349
Percent Similarity: 88.67% Conservative: 50
Best Local Similarity: 77.56% Mismatches: 50
Query Match: 79.71% Indels: 1
DB: 13 Gaps: 1
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US-10-614-954-6 (1-451) x US-10-074-279-11 (1-12949)

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QY 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21
Db 11282 TCTTTTGACATAGAGCTCGACATCATCGGCCAGCAACCGCTCTTCTTCAATCTACACC 11341
QY 22 GlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThr 41
Db 11342 CAGATCAGTCTGTTTACCCCGTCTCTGATCCCTCCAGTATCCACCATCGTCAGCAC 11401
QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61
Db 11402 CTTGAGGAAGGCCATAAAGCGCTCTCTCAAACTTCCCATGGTCCGGGCCAGGTCAG 11461
QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81
Db 11462 ACCGAGGATCATCGCAAGAAACACAGAACTTCAAGATCAITTCATATGAGGAGACA 11521
QY 82 ProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet 101
Db 11522 CCCCCTGTTGGTGAAGACCTCCGCTGATGATTCCTCAGCGCCACGATCGAGGGGTG 11581
QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr 121
Db 11582 AGAAAGCGGGTTTCCCTTAGAGATGTTTGAAGAGAACCTCGCTCGCTCCGAGGAAGACA 11641
QY 122 LeuProIleGlyProGlyThrGlyProAspProLysProValIleLeuLeuGlnLeu 141
Db 11642 TTAGCTATCGACCTGGCAATGCCCAACGACCCAGAGCTGTGTGCTATTGCGAGCTC 11701
QY 142 AsnPheIleLysGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
Db 11702 AACTTCATTAAGGGCGGACTCAITTCACCGTCAACGGCAACATGGTGTATGGACATG 11761
QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr 181
Db 11762 ACAGCAAGATGCAATTATTCTCTTCTCAAGCGCTGCGCGCAACGAATCATTCACC 11821
QY 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsn 201
Db 11822 GAGGAGAAATCTCGGCCATGAACCTCGATCGCAAGACGGTAGTCCCTCTCTTGAANAAC 11881
QY 202 TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAsp 221
Db 11882 TACAAAGTTGGTCTCGAGCTAGACCAACCATCGATCGCCAAACCTGCGCTGCT--GGCGAC 11938
QY 222 AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet 241
Db 11939 GCTCCACCGCCAGCCCAAGCAAGCTGGGCGCTTCTTTTCATTCTCCCAAGGCCCTC 11998
QY 242 SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261
Db 11999 TCGAGCTGAAAGACGAGCCACAAAGACTCTTGACGCGCTGCTCCAAAGTTTGTCTCACT 12058
QY 262 AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle 281
Db 12059 GATGATGCTCTTTCGGCGTTTATCTGGCAATCAACCTCGCGCTAGCTCTCGCAAGATTG 12118
QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301
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Db	12119	GATGCTTCCACACCTACTGAATTTCTCCGCGCTGTGCGATCGGGGCCCAATGGGCGTA	12178
Qy	302	SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu	321
Db	12179	TCAAGCACATACCAGGCGCTTCTTCAAAACATGACCTCATGACTGACCGTGCCGGA	12238
Qy	322	IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla	341
Db	12239	ATCGCCAAACCACTTTGGCGCAACAGCATCAGCGCTCGGAACTCAACAGTGAT	12298
Qy	342	SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer	361
Db	12299	CGTTTGGCGACAGCAACACAAGCTTTGGCGCGTATCATGCTGGCTGCCTGACAAGTCG	12358
Qy	362	AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTyrAla	381
Db	12359	AGGCTCTCCCTGACCGCGAGTGGCAATCCGTCAAGCAGCATCATGCTGAGTTCCTGGGCC	12418
Qy	382	LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg	401
Db	12419	AAGGTGGATGCTGGGAGTATGACTTTGGGTTTGGACTGGGTAAAGCCTGAGAGTGTGAGA	12478
Qy	402	ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly	421
Db	12479	AGACCTCGCTTTGAACCTTTTGAGAGTTTGATGTACTTTATGCCCAAGACCGCTGATGGG	12538
Qy	422	GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys	441
Db	12539	GAGTTTACGGCGTCCATCTTCTGAGGGATGAGGATATGGAGAGACTAAAGCGGATGAG	12598
Qy	442	GluTrpThrLysTyrAlaGlnTyrValGly	451
Db	12599	GAGTGCACAAGTACGCAAGTATATTGGG	12628

RESULT 6

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RES001 8
US-10-614-954-11
; Sequence 11, Application US/10614954
; Publication No. US20040034884A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Ruznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/614,954
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 12949
; TYPE: DNA
; ORGANISM: Plasmid
US-10-614-954-11

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QY 382 LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg 401
Db 12419 AAGTGGGATGCTGGGAGTATGACTTTGGGTTGGAGCTGGTAAGCCTGAGAGTGTGAGA 12478
QY 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
Db 12479 AGACCTCGCTTGAACCTTTGAGAGTTGATGATCTTTATGCCCAAGAGCCTGATGGG 12538
QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441
Db 12539 GAGTTTACGGCGTCCATTCTCTGAGGATGAGGATATGAGAGACTAAGGCGGATGAG 12598
QY 442 GluTrpThrLysTyrAlaGlnTyrValGly 451
Db 12599 GAGTGACAAAGTACGCAAAAGTATATTGGG 12628

RESULT 7
US-10-074-279-10
; Sequence 10, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 13737
; TYPE: DNA
; ORGANISM: Plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-10-074-279-10

Alignment Scores:
Pred. No.: 1,13e-209 Length: 13737
Score: 1860.50 Matches: 349
Percent Similarity: 88.67% Conservatives: 50
Best Local Similarity: 77.56% Mismatches: 50
Query Match: 79.71% Indels: 1
DB: 13 Gaps: 1

US-10-614-954-6 (1-451) x US-10-074-279-10 (1-13737)
QY 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21
Db 51 TCTTTGACATAGAGCTCGACATCATCGCCAGCAACCGCTCTTCTTCAATCTACACC 110
QY 22 GlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThr 41
Db 111 CAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCAGTATCCCAACCATCGTCAGCACC 170
QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61
Db 171 CTTGAGGAAGGCTTAAAGCCCTCTCTCAAACTCCCATGGTCCGCGCCAGGTCAG 230
QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81
Db 231 ACCGAGGGCATCAGCGCAAGAAACACAGGAACCTTCCAAGATCATTCCATATGAGGAGACA 290
QY 82 ProArgValValValLysAspLeuArgAspProSerAlaProThrIleGluGlyMet 101
Db 82 ProArgValValValLysAspLeuArgAspProSerAlaProThrIleGluGlyMet 101
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Db 291 CCCGCTCTTGTGGTGAAGACCTCCGTGATGATTCTCTCAGCGCCACAGCATCGAGGGGTTG 350
QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr 121
Db 351 AGAAAGGCGGGTTTCCCTTAGAGATGTTTACGAGAAAGTCTCGCTCCGAGGAAAGACA 410
QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141
Db 411 TTAGCTATCGGACCTGGCAATGGCCCAACGACCCGAAAGCCTGTGTGTTATTTCGAGCTC 470
QY 142 AsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
Db 471 AACTTCATTAAAGGCGGACTCATTTCTACCGTCAACGGACACATGCTGCTATGGACATG 530
QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspPropheThr 181
Db 531 ACAGGACAAGATGCAATTATTCTCTCTCCAGGCGTCCGCAACGAATCATTTCAACC 590
QY 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsn 201
Db 591 GAGGAGGAAATCTCGGCCATGAACCTCGATCGCAAGACGGTAGTCCCTCTCTTTGAAAAC 650
QY 202 TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAsp 221
Db 651 TACAAGTTGGTCTCTGAGCTAGACCAACAGATCGCCAAACCTCGCGCTGCT---GGCGAC 707
QY 222 AlaValLeuThrProValSerAlaSerTyrAlaPhePheThrPheSerProLysAlaMet 241
Db 708 GCTCCACCCGACCGGCCCAAGCAAGCTGGCGGTTCTTTTTCATTCACTCCCAAGGCCCTC 767
QY 242 SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261
Db 768 TCGGAGCTGAAAGAGCGCAGCAAAAGACTCTTGACGCGTCTGTCGAAGTTTGTGTCAACT 827
QY 262 AspAspAlaLeuSerAlaPheIleTyrLysSerAlaSerArgValArgLeuGluArgIle 281
Db 828 GATGATGCTCTTTTCGGCGTTTATCTGGCAATCAACCTCGCGGTACTGCTCTCGCAAGATTG 887
QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301
Db 888 GATGCTTCCACACCTACTGAATTTGCGCGCTGTGACATGCGGGGCCCAATGGGCGTA 947
QY 302 SerAsnAsnTyrProGlyLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321
Db 948 TCAAGCACATATCCAGGCGCTTCTTCAAAACATGACCTACCATGACTCGACCGTCGCCGAA 1007
QY 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341
Db 1008 ATCCCAACGAACCACTTGGCGCAACAGCATCACGCTCGCTCGGAACCTCAACAGTGAT 1067
QY 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer 361
Db 1068 CGTTTGGCGAGACGACACAAAGCTTTGGCGACGTACATGATCGCTGCTGCAAGTCG 1127
QY 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381
Db 1128 AGCGTCTCCCTGACCGCGCATCGAATCGTCAAGCAGCATCATGCTGAGTTCTCTGGGCC 1187
QY 382 LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg 401
Db 1188 AAGGTGGGATGCTGGGAGTATGACTTTGGGTTGGACTGGGTAAGCCTGAGAGTGTGAGA 1247
QY 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
Db 1248 AGACCTCGCTTTGAACCTTTTGAAGTTTGAAGTTTGAAGTTTATGCCCCAAGAGCCTGATGG 1307
QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441
Db 1308 GAGTTTACCGCGCTCCATTCTCTGAGGATGAGGATATGAGAGACTAAGGCGGATGAG 1367
QY 442 GluTrpThrLysTyrAlaGlnTyrValGly 451
Db 1368 GAGTGACAAAGTACGCAAAAGTATATTGGG 1397
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RESULT 8

US-10-614-954-10
; Sequence 10, Application US/10614954
; Publication No. US2004003484A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/614,954
; CURRENT FILING DATE: 2003-07-07
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 13737
; TYPE: DNA
; ORGANISM: Plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-10-614-954-10

Alignment Scores:
Pred. No.: 1,13e-209 Length: 13737
Score: 1860.50 Matches: 349
Percent Similarity: 88.67% Conservative: 50
Best Local Similarity: 77.56% Mismatches: 50
Query Match: 79.71% Indels: 1
DB: 16 Gaps: 1

US-10-614-954-6 (1-451) x US-10-614-954-10 (1-13737)

QY	2	AlaPheIleGlnLeuLeuSerLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr	21
DB	51	TCCTTTGACATAGATCGACATCATCGCCAGCAACCGCCTCTCTTCAATCTACACC	110
QY	22	GlnIleSerLeuLeuTyrProValSerAspSerGlnTyrProThrIleValSerThr	41
DB	111	CAGATCAGTCTCTTTACCCGCTCTGATCCCTCCAGTATCCCAACCATCGTCAGCACC	170
QY	42	PheGlnGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLys	61
DB	171	CTTGAGGAAGGCTAAAGCGCTCTCTCAACCTTCCCATGGGTGCGCGGCCAGGTCAAG	230
QY	62	AlaGluGlyIleSerGluGlyAenThrGlyThrSerPheIleValProPheGluAspVal	81
DB	231	ACGAGGGCATCAGCGAAGAAACAAGAACTTCCCAAGATCATTCATATAGGAGACA	290
QY	82	ProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet	101
DB	291	CCCCGTCCTTGTGTGAAAGCTCCGTGATGATTCCTCAGCGCCACACGATCGAGGGGTG	350
QY	102	ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThr	121
DB	351	AGAAAGCGGGTTTCCCTTAGAGATGTTTACGAGAACGTCGTCGTCGAGGAAGACA	410
QY	122	LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu	141
DB	411	TTAGCTATCGGACCTGGCAATGCCCAACGACCGCCGAGCCTGTGTGTTATGACGTC	470
QY	142	AsnPheIleLysGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet	161
DB	471	AACTTCATTAAAGGCGGACATCTCTCAGCGTCAACGGACACATGCTGCTATGGACATG	530
QY	162	ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr	181

DB	531	ACAGGACAAGATGCAATTATTGCTCTCTCCAGGCGTGGCCGCAACGAATCATTCACC	590
QY	182	GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsn	201
DB	591	GAGGAGAAATCTGGCCATGAACCTCGATCGCAAGCGGTAGTCTCTCTCTTGAAAAC	650
QY	202	TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAsp	221
DB	651	TACAAAGTTGGTCTTGAGCTAGACCAACAGATCGCCAAACCTGGCGCTGCT---GGCGAC	707
QY	222	AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet	241
DB	708	GCTCCACCCGCGCACCGCCCAAGGCAAGCTGGGGTCTTTTTCATTCATCCCAAGGCCCTC	767
QY	242	SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr	261
DB	768	TCGGAGCTGAAAGACGCGCAAGACTCTTGACGCGTGTCCAAAGTTTGTGTCAACT	827
QY	262	AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle	281
DB	828	GATGATGCTCTTTGGCGTTTATCTGGCAATCAACCTCGCGGTACGCTCTCGCAAGATTG	887
QY	282	AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal	301
DB	888	GATGCTTCCACACCTACTGATTTCTGCCGCGTGTGACATCGCGGGCCCAATGGCGGTA	947
QY	302	SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu	321
DB	948	TCAGCACATATCCAGGCGCTTCTTCAAAACATGACCTACATGACTCGACCGTCCGCGAA	1007
QY	322	IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla	341
DB	1008	ATCGCAACGAACCACTTTCGCGCAACAGCATCACGCGCTCGGAACTCAACAGTGAT	1067
QY	342	SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer	361
DB	1068	CGTTTCGCGAGACGAAACACAGCTTTTGGCGAGCTACATCATGGCGCTGCTGACAAAGTCG	1127
QY	362	AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerTrpAla	381
DB	1128	ACGCTCTCCCTGACCGCGATCGAATCCGTCAAGCAGCATCATGCTGAGTTCCTGGGCGC	1187
QY	382	LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg	401
DB	1188	AAGTGGGATGCTGGGAGTATGATCTTGGTTTGGAGTGGTAAAGCTGAGAGTGTGAGA	1247
QY	402	ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly	421
DB	1248	AGACCTCGCTTTGAACCTTTTGAAGATTTGATGTACTTTATGCCCAAGAGCCTGATGG	1307
QY	422	GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys	441
DB	1308	GAGTTTACGGCGCTCATTTCTCTGAGGATGAGGATATGAGAGACTAAAGCGGATGAG	1367
QY	442	GluTyrThrLysThrAlaGlnTyrValGly	451
DB	1368	GAGTGACAAAGTACGCAAAAGTATATTGGG	1397

RESULT 9
US-10-074-279-7
; Sequence 7, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279

; CURRENT FILING DATE: 2002-02-12
 ; PRIOR APPLICATION NUMBER: US/09/538,414
 ; PRIOR FILING DATE: 2000-03-29
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 1425
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces cerevisiae
 US-10-074-279-7

Alignment Scores:
 Pred. No.: 4,26e-104 Length: 1425
 Score: 962.50 Matches: 202
 Percent Similarity: 62.86% Conservative: 84
 Best Local Similarity: 44.40% Mismatches: 158
 Query Match: 41.24% Indels: 11
 DB: 13 Gaps: 8

US-10-614-954-6 (1-451) x US-10-074-279-7 (1-1425)

QY 6 GlnLeuAspThrLeuGlyGlnLeuProGlyLeuSerIleTyrThrGlnIleSerLeu 25
 DB 64 CAATGTGATATTTGGGACACAACTTCGCTATACAACTATACACTCAATATGCTCT 123
 QY 26 LeuTyrProValSerAspSerGlnTyrProThrIleValSerThrPheGluGlnGly 45
 DB 124 ATCTCCGCTGACAGATCTTCTGCTCATGACCATATCGTAATACCTTTAACACAGGA 183
 QY 46 LeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLysAlaGluGlyIle 65
 DB 184 CTTGAACATTTGGCTAAATTTCCAGTGGCTAGCAGGAATGCTGTAATGAAGTGCT 243
 QY 66 SerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspValProArgValVal 85
 DB 244 GACGAGGTAACTGTTGACTACAGATTTGTCGCGCCACAAATTCCTCA---CTTATC 300
 QY 86 ValLysAspLeuArgAspProSerAlaProThrIleGluGlyMetArgLysAlaGly 105
 DB 301 GTCCAAAGATCTTCGAGAAGATCTGCTGCGCCCAACAATGGAATTCGCTTGAAGAGCTGAC 360
 QY 106 TyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThrLeu---ProIle 124
 DB 361 TTTCTATCTACATGTTAGACAAAGACTTTTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 125 GlyProGlyThrGly---ProAspAspProLysProValIleLeuLeuGlnLeuAsnPhe 143
 DB 421 GGAACACTATAGTATGGCGCCGACAGAGTGGCGCTGATTTGCGAGTTCAGCAAACTTT 480
 QY 144 IleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMetValGly 163
 DB 481 ATCTCCGGCGCTCGTCTTAATCTATGTCGGGACGACAAATATTATGGATATAACAGGA 540
 QY 164 GlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThrGluGlu 183
 DB 541 CAGGAAGATATCATCACTTGTCTCAATAATTTGCCACCAAAACCTTTTCTGATGAA 600
 QY 184 GluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsnTyrThr 203
 DB 601 GAATGCTCATTTGGAATATAGATAAAGCAATCTATCTTTGTTTGTATGAA---ACT 657
 QY 204 IleGlyProGluValAsp-----HisGlnIleValLysAla-----AspValAlaGly 219
 DB 658 TGGGAACCCGACACCGCTAGTTCATGAATATAGTGGAAACCTCTAGAAATACAGTGGA 717
 QY 220 GlyAspAlaValLeuThrProValSer---AlaSerThrAlaPhePheThrPheSerPro 238
 DB 718 GAGGAAAAGCAACAGCTCTTCTTCTTCGAATCTACTTGGGCTTATGTTGAATTTCTGCT 777
 QY 239 LysAlaMetSerGluLeuLysThrAspAlaAlaThrLysThrLeuAspAlaSerThrLysPhe 258
 DB 778 ATCTCATTTGAGAATCTGAGGATTTTGGCAATGACAGACATGTACTTCTGGCACAATAATTT 837

QY 259 ValSerThrAspAspAlaLeuSerAlaPheIleTyrLysSerAlaSerArgValArgLeu 278
 DB 838 GTCTCCACTGATGATATCGTCTGCTTTCATCTGGAATTCAGTTTCTCCAGCCCGTTTA 897
 QY 279 GluArgIleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAla 298
 DB 898 TCTGACTTAACACAGAAACGAATCAATTTAGGGCGTCTGCTGGATGTAGAAAACGG 957
 QY 299 MetGlyValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThr 318
 DB 958 CTAGGACTCCCGAAAACGATATCCAGGTTATTAGTCAACATGACCTTTAATACAGGTTC 1017
 QY 319 IleGlyGluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeu 338
 DB 1018 CTGAAAAGCTTGGATCATAAAGTTTGGGCGCTTCTTGCATCACAGATTCGACGAAAGCTA 1077
 QY 339 AspProAla-----SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsn 356
 DB 1078 GACCTTAAGTCTTCCGATTGGCTATATACATGCGCACTTCTGCTAGCTCCTTAGCCGA 1137
 QY 357 AsnProAspLysSerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMet 376
 DB 1138 TGCCCGGACAAAGACTAAGGTTTCTATACCTCAACCAATTCATCTTATCTGGAATATG 1197
 QY 377 LeuSerSerThrAlaLysValGlyLeuTyrAspTyrAspPheGlyLeuGlyLys 396
 DB 1198 GTCAGTTCTGGGCAAAAGTCAGCCTGTATGACGTTGATTCAATCTAGGCTTGGGAAG 1257
 QY 397 ProGluThrValArgArgProIlePheGluProValGluSerLeuMetTyrPheMetPro 416
 DB 1258 CCAAGAGTGTACAGCGCGCGCTTCATTTCCCTTGAGAGCTTATATATTTTATGCTCT 1317
 QY 417 LysLeuProAspGlyGluPheCysAlaLeuSerLeuArgAspGluAspMetArg 436
 DB 1318 AGATCTCCAGAGTGAATGGTGGTGGTCTTTTGGCTTAGAGATAAAGATTGGGAGTGC 1377
 QY 437 LeuLysAlaAspLysGluTyrThrLysTyrAlaGlnTyrValGly 451
 DB 1378 CTGAATGCGGATAAAGATGGACAAATTTATGCTACACATATAGGA 1422

RESULT 10

US-10-614-954-7
 ; Sequence 7, Application US/10614954
 ; Publication No. US20040034884A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hohn, T.
 ; APPLICANT: Salmeron, J.
 ; APPLICANT: Peters, C.
 ; APPLICANT: Kendra, D.
 ; APPLICANT: Reinders, J.
 ; APPLICANT: Kuznia, R.
 ; APPLICANT: Dill-Mackey, R.
 ; TITLE OF INVENTION: Transgenic Plant and Methods
 ; FILE REFERENCE: sequence list
 ; CURRENT APPLICATION NUMBER: US/10/614,954
 ; PRIOR FILING DATE: 2003-07-07
 ; PRIOR APPLICATION NUMBER: US/09/538,414
 ; PRIOR FILING DATE: 2000-03-29
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 1425
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces cerevisiae
 US-10-614-954-7

Alignment Scores:
 Pred. No.: 4,26e-104 Length: 1425
 Score: 962.50 Matches: 202
 Percent Similarity: 62.86% Conservative: 84
 Best Local Similarity: 44.40% Mismatches: 158
 Query Match: 41.24% Indels: 11
 DB: 16 Gaps: 8

US-10-614-954-6 (1-451) x US-10-614-954-7 (1-1425)

QY 6 GlnLeuAspThrLeuGlyGlnLeuProGlyLeuSerIleTyrThrGlnIleSerLeu 25
 DB 64 CAACCTTGATATTGTTGGACACAACTTCGCTATACAACTATACACTCAATATGCTCT 123

QY 26 LeuTyrProValSerAspSerGlnTyrProThrIleValSerThrPheGluGlnGly 45
 DB 124 ATCTACCGTGACCATCTCTCTCATGACCATATCGTAATATACCTTAAACAGAGGA 183

QY 46 LeuLysArgPheSerGluAlaValProThrValAlaGlyGlnValLysAlaGluGlyLe 65
 DB 184 CTTGAACACATTTGCTAAAATTTCCAGTGGCTAGCAGGAATGTCGTAATGAAGTGCT 243

QY 66 SerGluGlyAsnThrGlyThrSerPheIleValProPheGluAaspValProArgValVal 85
 DB 244 GACGAGGTAACACTGGTACCTACGAAATGTGCCGTGAGCAAAATTTCCA---CTTATC 300

QY 86 ValLysAspLeuArgAspProSerAlaProThrIleGluGlyMetArgLysAlaGly 105
 DB 301 GTCCAGAGCTTCGAGAGATCTGCTGCCCCCAACAATGGATTCGCTTGAAAGAGCTGAC 360

QY 106 TyrProMetAlaMetPheAspGluAsnIleLeuAlaProArgLysThrLeu---ProIle 124
 DB 361 TTTTCTTATCTACATGTTAGCAAAAGACTTTTGGCGCTTGCGATGACTATCAATCCACCT 420

QY 125 GlyProGlyThrGly---ProAspAspProLysProValIleLeuLeuGlnLeuAsnPhe 143
 DB 421 GGAACACATATAGTATGATGCCGCCCAAGAGTGGGCTGTATTTGGCAGTTTCAAGCAAACTTT 480

QY 144 IleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMetValGly 163
 DB 481 ATCTCGGGGGCTCGCTTAATCTATGTCGGGACGACCAATATATGGATATACACGGA 540

QY 164 GlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThrGluGlu 183
 DB 541 CAGGAAGTATCATCAACTTGCTCAATAAATCTGCCCAACCAAAACCTTTCTCTGTATGAA 600

QY 184 GluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsnTyrThr 203
 DB 601 GAACCTCTCATTTGGAATATAGATAAAAGCAAACTTATCTCTTTGTTGATGAA---ACT 657

QY 204 IleGlyProGluValAsp-----HisGlnIleValLysAla-----AspValAlaGly 219
 DB 658 TGGGAACCCGACACACCGCTAGTTTATGAATAGTGGAAACCTCTAGAAATACAGTGGGA 717

QY 220 GlyAspAlaValLeuThrProValSer---AlaSerTyrAlaPhePheThrPheSerPro 238
 DB 718 GAGGAAGAGGACAGCTGTTGTTCTTCGAACTCTACTTGGGCTTATGTTGAATTTTCTGCT 777

QY 239 LysAlaMetSerGluLeuLysAspAlaThrLysThrLeuAspAlaSerThrLysPhe 258
 DB 778 ATCTCAATTCGAAATCTGAGGATTTTGGCAATGACAGATGCTACTTCTGGCAACAAATTT 837

QY 259 ValSerThrAspAspAlaLeuSerAlaPheIleTyrLysSerAlaSerArgValArgLeu 278
 DB 838 GTCTCCACCTGATGATGCTGCTACTGCTTCTCATCTGGAATACAGTTTCTCGAGCCGGTGA 897

QY 279 GluArgIleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAla 298
 DB 898 TCTCGACTTAAACACGAGAAATCAAAATTTAGGCGCTGCTGGATGTTAGAAACGG 957

QY 299 MetGlyValSerAsnAsnTyrProGlyLeuGlnAsnMetThrTyrHisAsnSerThr 318
 DB 958 CTAGGACTTCCCGGAAACGATATCCAGGGTTATTAGTCAACATGACCTTTAATACAGGTTC 1017

QY 319 IleGlyGluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeu 338
 DB 1018 CTGAAAAGCTTGATCATAAAAGTTTGGCGGTTCTTGATCAGAGATTCGAGGAAGCTA 1077

QY 339 AspProAla-----SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsn 356

US-10-653-047-4594

QY 357 AsnProAspLysSerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMet 376
 DB 1138 TCCCGGACAGACTAAGTTTCTATACCTCAACCAATTTGATCTTATCTGGAATATG 1197

QY 377 LeuSerSerTyrAlaLysValGlyLeuTyrPheAspTyrAspPheGlyLeuGlyLys 396
 DB 1198 GTCAAGTTCGTGGCAAAAGTCAGCTGTATGACGTGATTCATCTCAATCTAGGCTTGGGAAG 1257

QY 397 ProGluThrValArgArgProIlePheGluProValGluSerLeuMetTyrPheMetPro 416
 DB 1258 CCCAAGAGTTGACGACGGCGCTTCATTTCCCTTGAGAGCTTAATATATTTATCGCT 1317

QY 417 LysLysProAspGlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArg 436
 DB 1318 AGATCTCCAGAGGTGAATGGTGGTGGTCTCTTTCCCTTAGAGATAAAGATTGGGAGTGC 1377

QY 437 LeuLysAlaAspLysGluTyrThrLysTyrAlaGlnTyrValGly 451
 DB 1378 CTGAATCGGATAGAAATGGTGGTGGTCTCTTTCCCTTAGAGATAAAGATTGGGAGTGC 1422

RESULT 11

US-10-653-047-4594

Sequence 4594, Application US/10653047

Publication NO. US20040229367A1

GENERAL INFORMATION:

APPLICANT: Randy M. Berka

APPLICANT: Michael W. Rey

APPLICANT: Jeffrey R. Shuster

APPLICANT: Sakari Kauppinen

APPLICANT: Ib Groth Clausen

APPLICANT: Peter Bjarke Olsen

TITLE OF INVENTION: Methods For Monitoring Multiple Gene

TITLE OF INVENTION: Expression

FILE REFERENCE: 5849.200-US

CURRENT APPLICATION NUMBER: US/10/653.047

CURRENT FILING DATE: 2003-08-29

PRIOR APPLICATION NUMBER: US/09/533.559

PRIOR FILING DATE: 2000-03-22

PRIOR APPLICATION NUMBER: 09/273.623

PRIOR FILING DATE: 1999-03-22

NUMBER OF SEQ ID NOS: 7860

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4594

LENGTH: 695

TYPE: DNA

ORGANISM: Aspergillus oryzae

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)-(695)

OTHER INFORMATION: n = A,T,C or G

US-10-653-047-4594

Alignment Scores:

Pred. No.: 6,34e-43 Length: 695

Score: 445.50 Matches: 97

Percent Similarity: 61.03% Conservative: 22

Best Local Similarity: 49.74% Mismatches: 67

Query Match: 18.09% Indels: 9

DB: 18 Gaps: 4

US-10-614-954-6 (1-451) x US-10-653-047-4594 (1-695)

QY 5 IleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThrGlnIleSer 24
 DB 117 GTAAAGCTGAACCTTCTGGGTGAGTGCCTGCC---CTCAGGATCTACAGCAATCTGC 173

QY 25 LeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThrPheGluGln 44
 DB 174 CTCTCTCTTCCGTTTCGATGCTCATCTGATCACC---GAGATAGTCAGAGCCCTAGAGAT 230

QY 45 GlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLysAlaGluGly 64


```

Db      231  GGCTCGAAGACTGTCACCAATTTCCCTGGGTAGCAGCAGATAGTCAGTGAAGGC 290
QY      65  IISerGluGlyAsnThrGlyThrSerPheileValProPheGluAspValProArgVal 84
Db      291  AGCAGCCACAAATCTCTGGCACAATTCATGATCAAGACACTGGGGAAGACTCCACCACCTG 350
QY      85  valValIysAspLeuArgAspProSerAlaProThrIleGluGlyMetArgLysAla 104
Db      351  GTTGTGAAGACTTCCGTATGATCCGACGTTCCGACCATGACGATTTGAGACGCGCC 410
QY      105  GlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThrLeuProIle 124
Db      411  GACTTTCCCTTCGGATGTTAGACGAGAACATATTGCTCTCGAAACCTTGCCA--- 467
QY      125  GlyProGlyThrGlyProAspPro-----LysProValIleLeuLeuGlnLeuAsn 142
Db      468  -----AGCCCTGACGAAGATATTATCTCACCGCGCTTCTTGTTCAGGCTAAT 515
QY      143  PheIleIysGlyLeuLeuLeuThrValAsnGlyGlnHisGlyAlaMetAspMetVal 162
Db      516  TWTATTACGGCGGCTGTGTCTCACTCTTTGTGGCCATCATAGACAATGGACATGACT 575
QY      163  GlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThrGlu 182
Db      576  GGTGANGGACAGGTATTACACTTCTCTGAGGAGATGTCGTGGGATACATATACAAGA 635
QY      183  GluGluMetThrAlaMetAsnLeuAspArgLysThrIleValPro 197
Db      636  TTGGAGCTAGAGTCAGGAGACTTAATGAAGGTCACTCGTCTCC 680

RESULT 12
US-10-425-115-160676
; Sequence 160676, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 160676
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_78117C.1
US-10-425-115-160676

Alignment Scores:
Pred. No.:      8,4e-12      Length:      2235
Score:          191.00      Matches:     110
Percent Similarity: 38.29%      Conservative: 60
Best Local Similarity: 24.77%      Mismatches: 219
Query Match:      8.18%      Indels:      55
DB:              18         Gaps:         16

US-10-614-954-6 (1-451) x US-10-425-115-160676 (1-2235)

QY      13  LeuProGlyLeuLeuSerIleThrGlnIleSerLeuLeuTyrProValSerAspSer 32
Db      463  CTCCTCATCATCACTTCTACACCAAGAGCTGCTCTGTACCGGCC-----GCC 516
QY      33  SerGlnTyrProThrIleValSerThrPheGluGlnGlyLeuLysArgPheSerGluAla 52
Db      517  CCCGACTTCCCGGACCGCTGGCGGCATGACGGCGCGCTGCCGACCGCTCCGCGTC 576
QY      53  ValProTrpValAlaGlyGlnValLysAlaGluGlyIleSerGluGlyAsnThrGlyThr 72
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Db      577  TTCTACCCCGCTCCCGCGCGCATCCCGCCAGGAC-----GACGGCGGC 618
QY      73  SerPheileValProPheGluAsp-ValProArgValValValIysAspLeuArgAspAs 92
Db      619  GCCTCGCGCTTGAGGCGCAGGAGGCGCGAGGTCTTCGAGCGCGGCGGCCGCGTC 678
QY      92  pProSerAla-ProThrIleGluGlyMetArgLysAlaGlyTyrProMetAlaMetPheA 112
Db      679  GCCTCGACGACCTCCCGGAGGGGACTCGCAGCGAGGC-----G 720
QY      112  spGluAsnIleIleAlaPro-----ArgLysThrLeuProIleGlyProGlyT 128
Db      721  GAGAAAGTCTTGACGACCTCTGTCGCGGTATACCGCGGTCTGAACTCTCGAGGGCCT--- 776
QY      128  hrdGlyProAspAspPro-LysProValIleLeuLeuGlnLeuAsnPheIleLysGly 147
Db      777  -----CCGCGCGCGCTTCTCGCGCTCAATTCACAAAGCTCAAGGCGGT 822
QY      148  LeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMetValGlyGlnAspAlaVal 167
Db      823  CTGGCGTGGGTGGCGCTTCAACACACGCGGTCTGACGCGCACCTCCACGTGCACATTC 882
QY      168  IleArgLeuLeuSerLysAlaCysArgAsnAspProPheThrGluGluMetThrAla 187
Db      883  ATGTCTCATGGCGGAGCTCTGCGCGGTATACCCCTGTCTGCTGACGCCCATTCACGAC 942
QY      188  MetAsnLeuAspArgLysThrIleValProTyrLeuGluAsnTyrThrIleGlyProGlu 207
Db      943  CGGTCTCTCTCGCTCCGTGCGGTG---CGCTGAGCTG-----CGGCG 987
QY      208  ValAspHisGlnIleValLysAlaAspValAlaGlyGlyAspAlaValLeuThrProVal 227
Db      988  TCGCGGAGGCGCCACGAGAAGACGACCGGCGGCGGCGGCGGCTGGTGCGC--- 1044
QY      228  SerAlaSerTrpAlaPhePheThrPheSerProLysAlaMetSerGluLeuLysAspAla 247
Db      1045  -----CGGTCTTCTGTTCCCGGAGCCACCTGTGCGCGCATCAAGGCGCG 1092
QY      248  AlaThrLysThrLeuAspAlaSerThrLysPheValSerThrAspAspAlaLeuSerAla 267
Db      1093  GCCAAGCGCGCTGCGCGCGCGGCGGCGGCGGCGGCTCTTCCAGTTCCTTGGGGCG 1152
QY      268  PheIleTrpLysSerAlaSerArgValArgLeuGluArgIleAspGlySerAlaPro--- 286
Db      1153  CATCTCTGGCGCGCTCTCCGCGCGCGG-----GGCTCGGCGCGCGC 1197
QY      287  -----ThrGluPheCysArgAlaValAspAlaArgProAlaMetGly-----ValSer 302
Db      1198  GACATCACCGCTTTCGCGCTTTCGCGGACTGCGCGCGCGCGCTCGACCGCGCTCCCG 1257
QY      303  AsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGluIle 322
Db      1258  CCGGCTTCTTCGGCAACCTCATCCAGGCGGTGTTCCAGGCGGTGCGCGGGGATGCTC 1317
QY      323  AlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAlaSer 342
Db      1318  CTGGGCGGCGCGCGGAGTGGCGCGGCTCTGCTGAGAGGCCATCGACGACGACGAC 1377
QY      343  MetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSerAsn 362
Db      1378  GCCGCGCGCTCACGAGGAGGTGGAGGAGTAC---GAGGCGCGCGCGCGGCTGTTCCAC 1434
QY      363  ValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerTrpAlaLys 382
Db      1435  TACAGC-----GACCGCGCGCGCGCAAC---TGGCTGCGCTCGGCGGCTCGCGCGC 1482
QY      383  ValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuProGluThrValArgArg 402
Db      1483  TTCAGGCTTACGACGTGCACTTC-----GGCTTCGAGCGCGCGCGGCTCGCGCAGC 1536
QY      403  ProIlePheGluProValGluSerLeuMetTyrPheMetPro---LysLysProAspGly 421
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Db	1537	GGCGGGAACAAGTTCGAGCGCATGGTACTGTACCCCGCCGCGGGGTGACGGC	1596
Qy	422	GlupheCysAlaLaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys	441
Db	1597	GGCATCGACGTCGAGCTGGCGCTGCACCGGAGCCATGCAGAGCTGGAGAAGGACGAC	1656
Qy	442	Glutrp	443
Db	1657	GACTTC	1662

RESULT 13

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US-10-437-963-75946
; Sequence 75946, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 75946
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_75986C.1
US-10-437-963-75946

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Alignment Scores:
Pred. No.:      1,01e-11      Length:      1341
Score:          187.50        Matches:     115
Percent Similarity: 37.12%    Conservative: 58
Best Local Similarity: 24.68% Mismatches:    188
Query Match:      8.03%      Indels:      105
DB:              17          Gaps:        25

US-10-614-954-6 (1-451) x US-10-437-963-75946 (1-1341)

Qy  21  ThrGlnIleSerLeuLeuTyr-----ProValSerAspSerSerGlnTyrProThr 37
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  118  ACGTACATCTCGGTGATATACGCTACCGCCACCGGCTCGGCCAAC-----165

Qy  38  IleValSerThrPheGluGlnGlyLeu---LysArgPheSerGluAlaValProThrVal 56
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  166  -----GCCGCCCTCGAGCGGGGGCTCGCAAGCGGCTGATCGAGTACCGCAGGTGG---216

Qy  57  AlaGlyGlnValLysAlaGluGlyIleSerGluGlyAsnThr-----70
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  217  GCAGCGGCCCTCGGCGTGGAGCGC-----GACGGCACCGGCCCATCTGCTCAACGAC 270

Qy  71  ---GlyThrSerPheIleValProPheGluAspValProArgValValLysAspLeu 89
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  271  GGGGGCGCGGTTGTCGAGGCGACGGCCGACGTCAGCTGCAGACGCTGATCGCGCTG 330

Qy  90  ArgAspAspProSerAlaProThrIleGluGlyMetArgLysAlaGlyTyrProMetAla 109
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  331  AAG-----CCGACGGCGGAG-----345

Qy  110  MetPheAspGluAsnIleIleAlaProArgLysThrLeuProIleGlyProGlyThrGly 129
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  346  -----GTGCTGAGGCTGCACCGG-----AGC 366

Qy  130  ProAspAspProLysProValIleLeuLeuGlnLeu---AsnPheIleLysGlyGlyLeu 148
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

367 GCGCAGCAGCCGGTGGAGCTGATGTCTATCTCAGGTACAGCGGTTCGCGTGCGCTCCCTC 426
149 IleLeuThrValAsnGlyGlnHisGlyAlaMetAspMetValGlyGlnAspAlaValile 168
::: :::
427 GTCTGGGCTTACCACGCAGCACATCGTGGCAGACGGCGGCCACCAACAACACTTTCTTC 486
ArgLeuLeuSerLysAlaCysArgAsn-----AspProPheThrGluGluMet 195
::: :::
487 CTCGCTGGAGCAGGCCACCGCGCGCGCGCTTCCACCTGTCTCCGTGTGACGACGCGC 546
ThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGlu-----Asn 201
::: :::
547 GTCTCTCTTCTCCGCGCGCGACACT-----CCCAAGSTCGAGTTCGAGCACCGCTGGC 600
TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspVallaglyGlyAsp 221
::: :::
601 GTGGAGTTCAAGCGGTACGACGACGACGAGGATGTCTCATCGCTCGCGCGCGCGCGAC 660
-----AlaValLeuThrProValSerAlaSerTipAlaPhePheThrPheSerPro 238
::: :::
661 GACGACGAGTGTGTATAAACAAGGTGCGACTTGAGCGCGGAATTC----- 705
LysAlaMetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPhe 258
::: :::
706 -----ATCTGAAGCTCAAGTCGACGGCGTGGCT-----GGCGCGCACCGCGC 750
ValSerThrAspAspAlaLeuSerAlaPheIleTyrLysSerAlaSerArgValArgLeu 278
::: :::
751 TACAGCAGCGTGCAGTGTGTTGGCGGCACCTGTGGCGATGATGACGAAGGACCGC--- 807
GluArgIleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAla 298
::: :::
808 ---GGGCTCGACGGGCGCGAGTCCACAGGCTGTGATCGCCGTTCGACGGGCGCGCGCG 864
MetGly-----ValSerAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsn 316
::: :::
865 ATGAGCCGCGCGTTCGGACGGCTACAGGGCAAATGCTGTCTCTGGCGCGCGCCAACC 924
SerThrIleGlyGluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSer 336
::: :::
925 GCACCGCGCGTGTGATGTCACCGCGCTGAAGCGCGCTGAGCGGTGAGTCTCAACCGG 984
GluLeuAspProAlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHis--- 355
::: :::
985 GAGGTG-----ATCCGGATCAACGACGGCTACTTCAAGTCGTTTCATCGACTTC 1032
AsnAsnProAspLysSerAsnValSerLeuThrAlaAspAlaAspPro----- 371
::: :::
1033 GCCAACTCCGCTCGGTGGAGGAGGACGGCTGTGTGCGCTCGCGCCACGCGCGGAGATG 1092
-----SerThrSerValMetLeuSerSerTipAlaLysValGlyLeuTrpAspTyrAsp 389
::: :::
1093 GTGCTGAGCCCGAACATCGNGGTGGACAGCTGCTGGGATCCGTTCTACGACCTCGAC 1152
PheGlyLeuGlyLeuGlyLysProGluThrValArgArgProIlePhe----- 405
::: :::
1153 TTCGGCGCGGG-----CGGCCATTCTTCTCATGCCCGCAGC 1188
GluProValGluSerLeuMetTyrPheMetProLys---LysProAspGlyGluPhe 423
::: :::
1189 TACTCTCGGTGTGAAGGTTTGCTCATCTCTGCTCGCGCTTCTTCGCGCGAGGACGGCTT 1248
CysAlaAlaSerLeuArgAspGluAspMetAspArgLeuLys----- 438
::: :::
1249 GACGCTAGTGTGCCACTCTTCACCGCGACATGACGCTCTTCAAGAACCTGCTGCTACTCA 1308
AlaAspLysGluTrpThr 444
::: :::
1309 TTCACAAAGACCAAACT 1326

1

RESIT.T 14

RESUL 14
US-10-424-599-66444

US-10-424-399-86444
: Sequence 66444. Application US/10424599

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; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 66444
; LENGTH: 1860
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_31012C.1
US-10-424-599-66444

Alignment Scores:
Pred. No.: 4,48e-10 Length: 1860
Score: 175.50 Matches: 103
Percent Similarity: 36.64% Conservative: 67
Best Local Similarity: 22.20% Mismatches: 183
Query Match: 7.52% Indels: 111
DB: 16 Gaps: 22

US-10-614-954-6 (1-451) x US-10-424-599-66444 (1-1860)

QY 21 ThrGlnIleSerLeuLeuTyrProValSerAspSerGlnTyrProThrIleValSer 40
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 197 TCCAAAGTGGAGCTGGTGGTCCGCC-----AATTCCACACGCGCCAGCGTCTATTTC 247

QY 41 ThrPheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlnVal 60
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 248 TATAGTCCAAATGGCGCCGCCAACCTTTTTCGAC-----GCCAAGGTT 289

QY 61 LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPhe----- 78
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 290 ATGAAGGAGGCACG-----ACCAAGGTGCTGGTGGCTTCTACCCA 331

QY 79 -----GluAspValProArgVal----- 84
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 332 ATGGTGGCGGCTCTCGCAGATGACGACGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 391

QY 85 -----ValValLysAspLeuArgAspPro 93
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 392 GGGGTGCTTTTCGTGGAGCGGACACTGGCGCGCTATCGACGATTTTCGGCGAT----- 445

QY 94 SerAlaProThrIleGluGlyMetArgLysAlaGlyTyrProMetAlaMetPheAspGlu 113
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 446 TTCGCTCCACACCTTGAG---CTCCGCCAGCTT---ATCCCGCGCGTGGATATTACCAA 499

QY 114 AsnIleAlaProArgLysThrLeuProIleGlyProGlyThrGlyProAspAspPro 133
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 500 GGAATAGCATCC----- 511

QY 134 LysProValIleLeuLeuGlnLeuAsnPheIleLys---GlyGlyLeuIleLeuThrVal 152
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 512 TATCCCTCTTGGTGTACAGGTAACACATTCAAATGTGGAGGGGTTCCTCGGGAGTT 571

QY 153 AsnGlyGlnHisGlyAlaMetAspMetValGlyGlnAspAlaValIleArgLeuLeuSer 172
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 572 GGTATGCACATCATGTACAGATGGAGCTCTGGTCTGCATCTTCATCATATCATGTGTA 631

QY 173 LysAlaCysArgAsnAspProPheThrGluGluGluMetThrAlaMetAsnLeuAspArg 192
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 632 GATGTGGCTCGT-----GGCTTGGAT--- 652

QY 193 LysThrIleValProTyrLeuGluAsnTyrThrIle-----GlyPro 206
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 653 GTTTCATTCACCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 712
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```
QY 207 GluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAspAlaValLeuThrPro 226
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 713 ATTTTGTATCATTAATACAAAGCCCCACAGCCATCAAGACTCAACAAGTACTAAT 772

QY 227 ValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMetSerGluLeuLysAsp 246
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 773 GCATCAGCAGCTGCTCTATTTTTCAGACTCACCGGTGACCACTGACACACTGA--- 839

QY 247 AlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThrAspAlaLeuSer 266
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 830 ---GCCAATCCAAAGAGATGGCAACACATCAGCTATAGTTCTTATGAGATGTTGGCG 886

QY 267 AlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIleGlySerAlaPro 286
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 887 GGTACAGTGTGGCGAAGTGTAAAGCAAGCAAGA-----GCATCTCTCATGATCAAGAA 940

QY 287 ThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyValSerAsnAsnTyrPro 306
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 941 ACCAAATTTGATCATTTGCAACTGATGAAGGTCAAGGTTGCAACCTCTTACCCCA---CCC 997

QY 307 GlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIle-----GlyGluIleAla 323
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 998 GGTACTTTGGCAATGTGATATTCAACACCACTATAGCTGTGGCAGGTGATCTGATG 1057

QY 324 AsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAlaSerMet 343
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 1058 TCAAAACCAACATGTTGTTGCTGCAAGCAGATCCACATGCAATG---TTA 1105

QY 344 ArgGlnArgThr-----ArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLys 360
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 1106 CGAATGGCAACAGATTTATTTGAGATCGGCTCTTGACTATCTAGAACTGCAACCCGATCTA 1165

QY 361 SerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrp 380
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 1166 AAAGCGTGGTTCGTGGGCTCATCTTCAAGTGTCAAACCTTGGTATCTACTAGCTGG 1225

QY 381 AlaLysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyProGluThrVal 400
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 1226 ACTAGCTTCCCAATCCATGATGCTGACTTGGTGGGA----- 1264

QY 401 ArgArgProIlePheGlu-----ProValGluSerLeuMetTyrPheMet 415
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 1265 ---AGGCCAATATTCTGGGACCTGGTGGAAATTCATACGAGGGGCTATCTTTTCATAAAT 1321

QY 416 ProLysLysPro---AspGlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMet 434
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 1322 CCAAGCTCAACCAATGATGGAGCTTCTGTGGCCATAGCTCTTCAGCTGACCATATG 1381

QY 435 AspArgLeuLys 438
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 1382 AAGCTGTTTAAAG 1393

RESULT 15
US-10-425-114-298
; Sequence 298, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 298
; LENGTH: 1753
; TYPE: DNA
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; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 700071662_FLI

US-10-425-114-298

Alignment Scores:

Pred. No.:	7,08e-10	Length:	1753
Score:	173.50	Matches:	98
Percent Similarity:	33.62%	Conservative:	59
Best Local Similarity:	20.99%	Mismatches:	157
Query Match:	7.43%	Indels:	153
DB:	16	Gaps:	19

US-10-614-954-6 (1-451) x US-10-425-114-298 (1-1753)

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QY 69 AsnThrGlyThrSerPheIleValProPheGluAspValProArgValValValLysAsp 88
   176 AACTCCAACTCGACCTCGTGGTGGCGGCTTCCACACGCCCGAGTGTCTACTTC-----229
   89 LeuArgAspAspProSerAlaProThrIleGluGly-----MetArg 102
   230 TACCGCGGACGCGCCCGTGGCGGGGGAGGGTTCTTCACGGCGAGCGTATGCGG 289
   103 LysAla-----GlyTyrProMetAla-----109
   290 CGCGCGCTGCGACAGGCGCTCGTGGCGTCTATCCCAATGGCGGGCGCTCGCGGGGAC 349
   109 -----109
   350 GAGGACGGTAGGTCGAGATCGACTGCAATGGCGAGGGAGTGTCTTCGTCGAGGCCGAC 409
   110 -----MetPheAspGluAsnIleAlaPro-----ArgLys 120
   410 GCGCCGATGCTCTGCGATGACTAGGCGTCTCGCGCCACCATGAGCTCAAGCGC 469
   121 ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuGln 140
   470 CTCATCCGACCGCTCGATTACCGACGACATCTCGCGCTTCGCGTACTCGTGTCCAG 529
   141 LeuAsnPheIleLys---GlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMet 159
   530 GTGACTATTTCAAATGTGGAGCGCTCCCTGGTGGCATGGCGATGCAACCATGACGCG 589
   160 AspMetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspPro 179
   590 GATGGCATGCTGGCTGCACTTCACTAATCATGCTGACCTCTGCGGTGA-----643
   180 PheThrGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeu 199
   643 -----643
   200 GluAsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGly 219
   644 GCTCAAATTTCTGTCATGCGCTTCATGACCGGACCGCCCTTCTTCGTGCT-----691
   220 GlyAspAlaValLeuThrProValSerAlaSerTyrAlaPhePheThrPheSerProLys 239
   692 -----CGTGNATCCACCACTCCATCTTTTCAACATATCGATACCAAGCT---736
   240 AlaMetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheVal 259
   737 -----GCCCGAGCTATGTTGTCCTCCACCAACCCAGTTCCCT 772
   259 -----259
   773 GCTTCCAAAGTCAAGCCACTGCGCTGTGGACATTTTCAAGCTCACTCGCTCAGAC 832
   260 -----SerThrAsp 262
   833 CTGGCGCGGCTGCGCTCACAGCTTCCTGCGAGGGAGGAGTGCACCCCGGTTTCAGCACATAT 892
   263 AspAlaLeuSerAlaPheIleThrLysSerAlaSerArgValArgLeuGluArgIleAsp 282
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Db 893 GCAGTGCTAGCGGCACATGTCGTGAAATGTGTCTCCCTTGACAGC-----AGCTACTCT 946
QY 283 GlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMet-----Gly 300
Db 947 CTTGACACACCCCAAGTTGTTGCGCCACTGACGCCCGCACACGCGTACAGCTCCA 1006
QY 301 ValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIle---319
Db 1007 CTACAGATGGGTACTTTTGGC-----AATGTCACTCTTCCACCGCACACCACTTGT 1057
QY 320 -----GlyGluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGlu 337
Db 1058 GAGCGCGGCAAGTGACCAAGTGAG---CTGGCAGAGGAGGAGCAGTATCCAGGAGCA 1114
QY 338 LeuAspProAlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsn 357
Db 1115 CTGGATAGATGGAC---AACGACTACTGCGCTCAGCGTTAGACTACTCTGGAGCTTCAA 1171
QY 358 ProAspLysSerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeu 377
Db 1172 CCGGATCTGTCAACACTTGTGCGTGGAGCGCATACCTTCCGCTGCCCGAACCTAGGGCTC 1231
QY 378 SerSerTyrAlaLysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysPro 397
Db 1232 ACCAGCTGGGTGCGCTTCCTATCCATGCTGACTTCGGATGGGC-----1279
QY 398 GluThrValArgArgProIlePheGlu-----ProValGluSerLeuMet 412
Db 1280 -----CGGCTGTGTTTCATGGGGCCAGGTGGCATTGCGTATGAAGTCTGGCG 1327
QY 413 TyrPheMetProLys---LysProAspGlyGluPheCysAlaAlaLeuSerLeuArgAsp 431
Db 1328 TTTGTCTCTCCCAAGTGCAAAATGGCGACGCGACCTGTCCATTTGCTATCTCTGTTCAGAGCT 1387
QY 432 GluAspMetAspArgLeuLys 438
Db 1388 GAGCACATGGAGAAGTTCCGG 1408
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Search completed: January 24, 2005, 10:54:26

Job time : 814 secs